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OM nucleic - nucleic search, using sw model

Run on: December 27, 2002, 00:13:34 ; Search time 9586 Seconds
(without alignments)
17560.049 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

Database : GenEmbl:

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- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

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and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	5784	100.0	5784	6	AX330488	AX330488 Sequence
2	5784	100.0	5784	6	AX375587	AX375587 Sequence
3	5784	100.0	5784	6	AX409513	AX409513 Sequence
4	5784	100.0	5784	6	AX480837	AX480837 Sequence
5	5784	100.0	5784	9	HUMTHRSPO	L12350 Human thrm
6	2830.8	48.9	4697	4	BTHROM2	X96340 B.taurus mr
7	2778	48.0	2780	9	HUMTHRSPD	M81339 Human thrm
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9	2023.2	35.0	3537	5	CHKTHBSA	M60853 Chicken thr
10	1985	34.3	2026	11	G06722	G06722 human STS W
11	1872	32.4	2837	10	MUSTHBS2	M64866 Mouse thrm
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13	1550.4	26.8	5722	6	AX094823	AX094823 Sequence
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20	1522.2	26.3	4339	10	MUSTSP1A	M87276 Mouse thrm
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22	1139.4	19.7	1559	4	BTRNAT3	X87620 B.taurus mr
23	904	15.6	2162	4	BTRNAT1	X87618 B.taurus mr
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ALIGNMENTS

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LOCUS AX330488 5784 bp DNA linear PAT 09-JAN-2002
DEFINITION Sequence 997 from Patent WO0194629.
ACCESSION AX330488
VERSION AX330488.1 GI:18103466
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrikan, S., Soppet, D.R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature

gene sets
JOURNAL Patent: WO 0194629-A 997 13-DEC-2001;
Avalon Pharmaceuticals (US)
FEATURES Location/Qualifiers
source 1..5784
BASE COUNT 1447 a 1460 c 1518 g 1359 t
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 5784; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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REFERENCE
AUTHORS      Bornstein,P., Kyriakides,T., Ratner,B., Giachelli,C.,
              Martinson,L.D. and Scatena,M.
TITLE        Methods and devices to modulate the wound response
JOURNAL      Patent: WO 0209735-A 3 07-FEB-2002;
              The University of Washington (US)
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AX480837
LOCUS AX480837 5784 bp DNA linear PAT 12-AUG-2002
DEFINITION Sequence 3 from Patent WO0239122.
ACCESSION AX480837
VERSION AX480837.1 GI:22217528
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 McCarthy J.
AUTHORS
TITLE Compositions and methods for the identification, assessment,
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JOURNAL Patent: WO 0239122-A 3 16-MAY-2002;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
Location/Qualifiers
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/db_xref="taxon:9606"
BASE COUNT 1447 a 1460 c 1518 g 1359 t
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Query Match 100.0%; Score 5784; DB 6; Length 5784;
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Db 1 ACGGCATCCAGTACAGAGGGGCTGGACTTGGACCCCTGCAGCAGCCCTGCACAGGAGAAG 60
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Db 61 CGGCATATAAGCCCGCTGCCGGAGCCGCTCGGCCACGTCACCGAGCATCCTGCA 120
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Db	361	GCGCCAAGCAGTTTCGGGGGGCCGACCCCGGGCGTTCGGGCTTACGCGTTCGTGGCGCTTTG	420
	421	ACTACATCCCAACCGGTGAACGCAGATGACCTCAGCAAGATCACCAAGATCATATGGCGAGA	480
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	481	AGGAGGGCTTCTTCCTCAGGGCCAGCTCAAGCAGGACGGCAAGTCCAGGGGACACGCTGT	540
Qy	541	TGCTCTGGAGGGCCCGGCTCTCCCAAGAGCAGTTTCGAGATCGTCTCCAAACGGGCCCG	600
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Qy	661	ACGTTCGGCTTGGCTGACTCGCAGTGAAGAACGTCACCGTGCAGTGGCTTTCACGAGACCT	720
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Qy	721	ACAGCTTGACAGTGGGCTGGACCTCATAGGACCAAGTTGCTCTGGACGAGCCCTTCTACG	780
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Qy	1081	CGGGCTTCCACGCTCTCTGTAACAGCTCAGGAGAACCTCAAGAGAGTGTGCAATGATA	1140
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	1141	ACCAGTTTCTCTGGAGCTCATTTGGTGGCCCTCCCTAAGCAAGGAACATGTACGCTTGCT	1200
Qy	1201	GGCAGATGCGCGGTTCTTGGGAAATGAAACGCTGGTGGAGACAGCTGCACACAGT	1260
	1201	GGCAGATGCGCGGTTCTTGGGAAATGAAACGCTGGTGGAGACAGCTGCACACAGT	1260
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	1321	CCAGTCCATCTTTGTGGAAGCGAATGTCGCCCTTCTGCTCCACTCGGTGGACGGTG	1380
Qy	1381	AGGAGGGCTGCTCCGTGGGAGAGTGACCCAGTGTCCGTGACGTGTGGCTCTGGGA	1440
	1381	AGGAGGGCTGCTCCGTGGGAGAGTGACCCAGTGTCCGTGACGTGTGGCTCTGGGA	1440

QY	1441	CCAGCAGAGAGCGCGTCTCTGTGAGTGCACAGCAACACCTGCTGTGGGGCCCTCGATCC	1500
DB	1441		
		CCACAGCAGAGCGCGTCTCTGTGAGTGCACAGCAACACCTGCTGTGGGGCCCTCGATCC	1500
QY	1501	AGACACGGCTTGCACTGTCAGCAAGTGTGACACCCGCATCCGGCAGGACGCGCGCTGGA	1560
DB	1501		
		AGACACGGCTTGCACTGTCAGCAAGTGTGACACCCGCATCCGGCAGGACGCGCGCTGGA	1560
QY	1561	GCCACTGGTCACTTGGTCTTTCATGTCTGTGACCTGTGTGAGTTTGGCAATATCAACGCA	1620
DB	1561		
		GCCACTGGTCACTTGGTCTTTCATGTCTGTGACCTGTGTGAGTTTGGCAATATCAACGCA	1620
QY	1621	TCCGTCTCTGCAACTCCCACTGCCAGTGCCTCCAGATGGGGGGCAAGAATTGCAAAAGGAGTGCC	1680
DB	1621		
		TCCGTCTCTGCAACTCCCACTGCCAGTGCCTCCAGATGGGGGGCAAGAATTGCAAAAGGAGTGCC	1680
QY	1681	GGGAGACAAAGCCTGCCAGGCGCCCATGCCCAATCGATGGCGCTGGAGGCCCTCGT	1740
DB	1681		
		GGGAGACAAAGCCTGCCAGGCGCCCATGCCCAATCGATGGCGCTGGAGGCCCTCGT	1740
QY	1741	CCCGTGTGTGGCGCTGCACCTGTCCACTGTGCCGTGGGATCCGGGAGGCGCACCCGGGTCT	1800
DB	1741		
		CCCGTGTGTGGCGCTGCACCTGTCCACTGTGCCGTGGGATCCGGGAGGCGCACCCGGGTCT	1800
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DB	1801		
		GCAACAGCCCTGAGCCTCACTAGTACGGAGGGAAGCCCTGCTGGGGGATGTGACGAGAGCTC	1860
QY	1861	AGATGTGCACAAGAGAGAGCTGCCCGTGGATGGCTGTTTATCCAAACCCTGCTTCCCGG	1920
DB	1861		
		AGATGTGCACAAGAGAGAGCTGCCCGTGGATGGCTGTTTATCCAAACCCTGCTTCCCGG	1920
QY	1921	GAGCCAGTGCAGCAGCTTCCCGATGGGTCTCTGTGCTCATGCGGCTTCTGCCCTGTGGGCT	1980
DB	1921		
		GAGCCAGTGCAGCAGCTTCCCGATGGGTCTCTGTGCTCATGCGGCTTCTGCCCTGTGGGCT	1980
QY	1981	TCTTGGGCAATGGAACCCACTGTGAGGACCTGTGACGAGTGTGCCCTGTGTCCCGACACT	2040
DB	1981		
		TCTTGGGCAATGGAACCCACTGTGAGGACCTGTGACGAGTGTGCCCTGTGTCCCGACACT	2040
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DB	2041		
		GCTTCTCCACAGCAAGTGCCTCGCTGTGTCAACACTCAGCCTGCTGCTTCCACTGCTCTGC	2100
QY	2101	CCTGCCGCCCCGATACAGAGGAAACACGCCCTCGGGTTCGGCTTGAAGCAGCCAAGA	2160
DB	2101		
		CCTGCCGCCCCGATACAGAGGAAACACGCCCTCGGGTTCGGCTTGAAGCAGCCAAGA	2160
QY	2161	CGGAAAGCAAGTGTGTGAGCGCGAAACCCATGCAAGGACAAACACAACTGCCACA	2220
DB	2161		
		CGGAAAGCAAGTGTGTGAGCGCGAAACCCATGCAAGGACAAACACAACTGCCACA	2220
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DB	2221		
		AGCAGCGGAGTGCACTACCTGGGTCACTTCAGCGACCCCATGTACAAGTCCGAGTGCC	2280
QY	2281	AGACAGGCTACGCGGGCAGCGGCTCATCTTGGGGGAGGACTCGGACCTTGGAGGCTGGC	2340
DB	2281		
		AGACAGGCTACGCGGGCAGCGGCTCATCTTGGGGGAGGACTCGGACCTTGGAGGCTGGC	2340
QY	2341	CCAACTCAATCTGGTCTGCCCAACCAAGCCACCTTACCACCTGCATCAAGGATAACTGCC	2400
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DB	2401		
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DB	2461		
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AUTHORS	Feige,J.J.
TITLE	Direct Submission
JOURNAL	Submitted (08-MAR-1996) J.J. Feige, Inserm U 244, DBMS/BRCB, CEA/Grenoble, 17 rue des Martyrs, F-38054 Grenoble Cedex 9, France revised by [3]
REMARK	3 (bases 1 to 4697)
AUTHORS	Feige,J.J.
TITLE	Direct Submission
JOURNAL	Submitted (19-MAR-1998) J.J. Feige, Inserm U 244, DBMS/BRCB, CEA/Grenoble, 17 rue des Martyrs, F-38054 Grenoble Cedex 9, France
COMMENT	On Mar 28, 1998 this sequence version replaced gi:2695840.
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ORGANISM Homo sapiens
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REFERENCE 1 (bases 1 to 2780)
AUTHORS LaBell,T.L., Milewicz,D.J., Distche,C.M. and Byers,P.H.
TITLE Thrombospondin II: partial cDNA sequence, chromosome location, and
expression of a second member of the thrombospondin gene family in
humans
JOURNAL Genomics 12 (3), 421-429 (1992)
MEDLINE 9221961
PUBMED 1559694
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Qy	3536	CAGGAACATTGGCTGGAAGGACTACACGGCTATAGTGTGGCACCTGACTCACAGGCCCAA	3595
Db	1621	CAGGAACATTGGCTGGAAGGACTACACGGCTATAGTGTGGCACCTGACTCACAGGCCCAA	1680
Qy	3596	GACCGGTACATCAGAGTCTTAGTGATGCAAGGAANAACAGGTCATGGCAGACTCAGGACC	3655
Db	1681	GACCGGTACATCAGAGTCTTAGTGATGCAAGGAANAACAGGTCATGGCAGACTCAGGACC	1740
Qy	3656	TATCTATGACCAAACTACGCTGGCGGGCGGCTGGGTCTATTTGCTCTCTCTCAAGAAT	3715
Db	1741	TATCTATGACCAAACTACGCTGGCGGGCGGCTGGGTCTATTTGCTCTCTCTCAAGAAT	1800
Qy	3716	GGTCTATTCTCAGACCTCAAGTACGAATGACAGATATTTAAACACAGATTTTGTGCATT	3775
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Qy	3776	TCGGGCAATGCCCTGTGCATGCCATGGTCCCTTAGACACCTCAGTTCTATGTGGTCTTGC	3835
Db	1861	TCGGGCAATGCCCTGTGCATGCCATGGTCCCTTAGACACCTCAGTTCTATGTGGTCTTGC	1920
Qy	3836	GGCTTCTCTCTTAGCAGCACCTCCTGTCCCTTGACCTTAACTCTGATGTTCTTCCACCT	3895
Db	1921	GGCTTCTCTCTTAGCAGCACCTCCTGTCCCTTGACCTTAACTCTGATGTTCTTCCACCT	1980
Qy	3896	CCTGGCCAGCAACCCCAAAACCAAGTGGCTTCAGAGGATAAATCAATGAACCTCAGAGA	3955
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Qy	4016	AAAAATTGGGCATGCCATTACATTCGTTTTCTTGTGTTTAAAAAAGAAATGACGTTTACA	4075
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Db			
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Db	2701	TGAGAGGAACACAGACGACGACACAGGCGGAAAAGGCGCATCTTAAGCGCTATCTAGGCT	2760
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Db			
Db	2761	TTGTTAACTCGGGACAAG	2778

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RESULT 8
LOCUS MUSTSP2B
DEFINITION Mus musculus thrombospondin 2 (THBS2) mRNA, complete cds.
ACCESSION L07803 MB7275
VERSION L07803.1 GI:340421
KEYWORDS thrombospondin 2.
SOURCE Mus musculus.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 4108)
AUTHORS Laherty,C.D., O'Rourke,K., Wolf,F.W., Katz,R., Seldin,M.F. and
Dixit,V.M.
TITLE Characterization of mouse thrombospondin 2 sequence and expression
during cell growth and development
JOURNAL J. Biol. Chem. 267 (5), 3274-3281 (1992)
MEDLINE 92147683
PUBMED 1371115
COMMENT On Feb 8, 2002 this sequence version replaced gi:202198.
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ORIGIN
Query Match      47.5%; Score 2745.2; DB 10; Length 4108;
Best Local Similarity 82.5%; Pred. No. 0;
Matches 3218; Conservative 0; Mismatches 673; Indels 9; Gaps 6;
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QY 586 TCTCAACGGCCCGCGGACACGCTGGATCTACCTTACTTGATTTAGCGCACCCCGCATG 645
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QY 646 TGGTCTCCCTGGAGGACGTCGCGCTGGCTGACTCGCAGTGGAGAACGTCACCGTGCAGG 705
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Qy	2806	ACCAGTGTGACAACAACGAGGACATAGATGACGCGGCCACCGAACAACACGAGACAACCT	2865
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RESULT 9	CHKTHBSA	3537 bp	mrna	linear	VRT 30-OCT-1994		
LOCUS	Chicken thrombospondin mRNA, complete cds.						
DEFINITION	M60853						
ACCESSION	M60853.1	GI:212763					
VERSION							
KEYWORDS	thrombospondin.						
SOURCE	Chicken, cdna to mRNA.						
ORGANISM	Gallus gallus						
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.						
REFERENCE	1 (bases 1 to 3537)						
AUTHORS	Lawler, J., Duquette, M. and Ferro, P.						
TITLE	Cloning and sequencing of chicken thrombospondin						
JOURNAL	J. Biol. Chem. 266 (13), 8039-8043 (1991)						
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PUBMED	2022631						
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ORIGIN							
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RESULT 10
LOCUS G06722 2026 bp DNA linear STS 19-OCT-1995
DEFINITION human STS WI-7830, sequence tagged site.
ACCESSION G06722
VERSION G06722.1 GI:859967
KEYWORDS STS; STS sequence; primer; sequence tagged site.
SOURCE Homo sapiens STSs derived from sequences in dbEST and the Unigene collection.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2026)
AUTHORS Hudson,T.
TITLE Whitehead Institute/MIT Center for Genome Research; Physically
MAPPED ESTs
JOURNAL Unpublished (1995)
COMMENT
Contact: Thomas Hudson
Whitehead Institute/MIT Center for Genome Research
Whitehead Institute for Biomedical Research
9 Cambridge Center, Cambridge MA 02142 USA
Tel: 617 252 1900
Fax: 617 252 1902
Email: thudson@genome.wi.mit.edu

Primer A: GCAGGAATAGTCACTCATCCC
Primer B: TTGACCCCAACACAGAAA
STS size: 347
PCR profile:
  Denaturation:
    Annealing: 56 degrees C
    Polymerization:
      PCR Cycles: 35
      Thermal Cycler:
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          Primer: each 5 pM
          dNTPs: each 4 mM
          Taq Polymerase: 0.025 units/ul
          Total Vol: 20 ul

Buffer:
  MgCl2: 1.5 mM
  KCl: 50 mM
  Tris-HCL: 10 mM
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Prepared with primer pairs derived from L12350 -- Unigene.
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AUTHORS	Bornstein, P., O'Rourke, K., Wikstrom, K., Wolf, F.W., Katz, R., Li, P.		
TITLE	A second, expressed thrombospondin gene (Thbs2) exists in the mouse genome		
JOURNAL	J. Biol. Chem. 266 (20), 12821-12824 (1991)		
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AB005287

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REFERENCE

AB005287 5269 bp mRNA linear MAM 20-APR-1999
Bos taurus mRNA for thrombospondin 1, complete cds.
AB005287
AB005287.2 GI:4630795
thrombospondin 1.
Bos taurus (strain:Holstein) two weeks after birth male anterior
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Bos taurus
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (sites)
Ueno,A., Yamashita,K., Nagata,T., Tsurumi,C., Miwa,Y., Kitamura,S.
and Inoue,H.
cDNA cloning of bovine thrombospondin 1 and its expression in
odontoblasts and preodontoblasts
Biochim. Biophys. Acta 1382 (1), 17-22 (1998)
98173773
2 (bases 1 to 5269)
Ueno,A.
Direct Submission
Submitted (30-JUN-1997) Akemichi Ueno, The University of Tokushima,
Department of Biochemistry, School of Dentistry; Kuramoto-cho
3-18-15, Tokushima, Tokushima 770, Japan
(E-mail:akemichi@dent.tokushima-u.ac.jp, Tel:++81-886-33-7326,
Fax:++81-886-31-4215)
On Apr 21, 1999 this sequence version replaced gi:2244706.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 5722)
AUTHORS Lander, E.S., Gargill, M., Ireland, J.S., Bolk, S., Daley, G.O. and
McCarthy, J.J.

TITLE Single nucleotide polymorphisms in genes
JOURNAL Patent: WO 0118250-A 1 15-MAR-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US); Millennium
Pharmaceuticals, Inc. (US)
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Alvares,C., Horne,D., Peres-da-Silva,S. and Vockley,J.G.
Gene expression profiles in liver cancer
Patent: WO 0229103-A 3704 11-APR-2002;
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QY 492 TTCCCTCAGCGCCACGCTCAAGCAGGACGCAAGTCCAGGGGACGCTGTTCGCTCTGGAG 551
Db 376 CTCTCTTGGCATCTCCTGAGGAGATGAAGAAGACCGGGGACGCTGTGCGCCCTGGAG 435
QY 552 GGCCCGGCTCTCTCCAGAGGAGTTCAGAGATCTCTCCACGGGCGCCGACACCGTGTG 611
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Search completed: December 27, 2002, 03:13:33
Job time : 9631 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 27, 2002, 00:12:49 ; Search time 725 Seconds

(Without alignments)

17966.287 Million cell updates/sec

Title: US-09-919-770-3

Perfect score: 5784

Sequence: 1 acggcatccagtcacagagg.....aattgtaaaaagggtttct 5784

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
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- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
- 24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5784	100.0	5784	24	Gene #2160 used to
2	5784	100.0	5784	24	Human cDNA encodin
3	5784	100.0	5784	24	Colon adenocarcino
4	3683.4	63.7	3787	21	Human cancer assoc
5	3573.6	61.8	3596	21	Human thrombospond
6	3404.8	58.9	3522	22	Human colon cancer
7	2745.2	47.5	4108	22	Human METH1 relate
8	2745.2	47.5	4108	22	L07803 CDNA clone.
9	2731.8	47.2	4170	24	Rat cDNA isolated

10	1872	32.4	2837	20	AAZ320015	Human METH1 relate
11	1872	32.4	2837	22	AAZ90072	M64866 CDNA clone.
12	1604.2	27.7	5289	20	AAZ320052	Human METH2 relate
13	1604.2	27.7	5289	22	AAZ90309	AB005287 CDNA clon
14	1550.4	26.8	5721	22	AAH02923	Human shear stress
15	1550.4	26.8	5722	20	AAZ32012	Human METH1 relate
16	1550.4	26.8	5722	22	AAZ95238	Human variant thro
17	1550.4	26.8	5722	22	AAZ90069	X14787 CDNA clone.
18	1550.4	26.8	5722	22	AAZ97206	Gene #3704 used to
19	1548.8	26.8	4433	20	AAZ32014	Human METH1 relate
20	1548.8	26.8	4434	22	AAZ90071	X04665 CDNA clone.
21	1548.8	26.8	6132	23	ABV24661	Human prostate exp
22	1548.8	26.8	7232	24	AAZ94912	Human DNA sequence
23	1529.8	26.4	5830	21	AAZ77811	Human cancer assoc
24	1522.2	26.3	4339	20	AAZ32054	Human METH2 relate
25	1522.2	26.3	4339	22	AAZ90311	M87276 CDNA clone.
26	684.6	11.8	2468	22	AAZ90613	Angiotensin conver
27	651.8	11.3	713	22	AAH34534	Human colon cancer
28	601.6	10.4	2439	24	ABL62104	Colon adenocarcino
29	601.6	10.4	2439	24	ABL62870	Breast cancer rela
30	601.6	10.4	2439	24	ABL63089	Breast cancer rela
31	595.6	10.3	619	21	AAZ78040	CDNA encoding huma
32	595.6	10.3	619	22	AAZ28778	Colon tumour relat
33	594.8	10.3	848	20	AAZ17196	Human gene express
34	566.6	9.8	2563	22	AAZ94355	Human full-length
35	559.4	9.7	3074	15	AAZ66455	Human thrombospond
36	559.4	9.7	3074	24	ABL69126	Kidney cancer rela
37	559.4	9.7	3434	22	AAZ95239	Human variant thro
38	545.6	9.4	2916	22	AAZ52211	Human polynucleoti
39	540.2	9.3	637	23	AAZ58772	CDNA #1448 encodin
40	526.4	9.1	2820	15	AAZ66454	Xenopus thrombospo
41	526	9.1	2053	20	AAZ32053	Human METH2 relate
42	526	9.1	2053	22	AAZ90310	X87619 CDNA clone.
43	516	8.9	516	24	ABK45682	CDNA encoding colo
44	514.6	8.9	925	21	AAA47735	Human COMP/TSP-2 c
45	496.6	8.6	1516	21	AAZ21836	Human breast and o

ALIGNMENTS

RESULT 1

ABN95662
ID ABN95662 standard; DNA; 5784 BP.

AC ABN95662;

DT 13-AUG-2002 (first entry)

DE Gene #2160 used to diagnose liver cancer.

Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;
metastatic liver tumor; cytostatic; expression profile; disease state;
disease progression; drug toxicity; drug efficacy; drug metabolism.

OS Homo sapiens.

PN WO200229103-A2.

PD 11-APR-2002.

PF 02-OCT-2001; 2001WO-US30589.

PR 02-OCT-2000; 2000US-237054P.

PA (GENE-) GENE LOGIC INC.

PI Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;

DR WPI; 2002-426119/45.

PT Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient,


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Db 3961 ATCTAACCCACTAGAGGAACAGTTGGTGATATATGAGACTTTATGTGAGTGAAAAAT 4020
Qy
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Db 4021 TGGGCATGCCATTACATTCGTTTTCTTGTTGTTTAAAGAAAGATGAGCTTTACATATAA 4080
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Db 5101 AATCAGTCATGTGTAATATGACAAAGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTG 5160
Qy
|||||
Db 5161 TTTTGTGTTTAAAGTTGTCATGATCTTCTGTCAGGAAATAGTCACTCATCCACCCACAT 5220
Qy
|||||
Db 5161 TTTTGTGTTTAAAGTTGTCATGATCTTCTGTCAGGAAATAGTCACTCATCCACCCACAT 5220
Qy
|||||
Db 5221 AAGGGGTTTAAAGAGAGAGTCTGCTGCTGATGATGATGAGGGGCAAAATCTTTTTC 5280
Qy
|||||
Db 5221 AAGGGGTTTAAAGAGAGAGTCTGCTGCTGATGATGATGAGGGGCAAAATCTTTTTC 5280
Qy
|||||
Db 5281 CCTTCTGTTTAAATAGTCATCACTTCTATGCCAAACAGGAAACGATCATCACTTTAGTC 5340
Qy
|||||
Db 5281 CCTTCTGTTTAAATAGTCATCACTTCTATGCCAAACAGGAAACGATCATCACTTTAGTC 5340
Qy
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Db 5341 TTAATGTACATTTGTCATTTTGTGATAAAATTAATTTGTTGTTTGTGTTTGTGTTTGTGTTTGTG 5400
Qy
|||||
Db 5341 TTAATGTACATTTGTCATTTTGTGATAAAATTAATTTGTTGTTTGTGTTTGTGTTTGTGTTTGTG 5400
Qy
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Db 5401 TGTCTGTTTGTGCTGCACTTTTACTTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5460
Qy
|||||
Db 5401 TGTCTGTTTGTGCTGCACTTTTACTTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5460
Qy
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Db 5461 AAGCGTTGGGATACCTTCATTAATGTAGCGACTGTCAACAGCGTGCAGGTTTCTGTTTC 5520
Qy
|||||
Db 5461 AAGCGTTGGGATACCTTCATTAATGTAGCGACTGTCAACAGCGTGCAGGTTTCTGTTTC 5520
Qy
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Db 5521 TGTCTGTTGGGCTCAACCGTACAAATGTTGGGAAATGACGATGATGTGAATATTAGAAT 5580
Qy
|||||
Db 5521 TGTCTGTTGGGCTCAACCGTACAAATGTTGGGAAATGACGATGATGTGAATATTAGAAT 5580
Qy
|||||
Db 5581 GTACCATATTTTGTAAATTTATTTATGTTTCTTAAACAAATTTATCGTATAGTTGAT 5640
Qy
|||||
Db 5581 GTACCATATTTTGTAAATTTATTTATGTTTCTTAAACAAATTTATCGTATAGTTGAT 5640
Qy
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Db 5641 GAAACGTCATGTGTTTGGCCAAAGACTGTAATATTTATTTATGTTTACATGTTCAAA 5700
Qy
|||||
Db 5641 GAAACGTCATGTGTTTGGCCAAAGACTGTAATATTTATTTATGTTTACATGTTCAAA 5700
Qy
|||||
Db 5701 ATTTTCAACCTGAAACCGTGCACCTAGTAGAACCTCATTTTAAAGATTTAAACACAGGA 5760
Qy
|||||
Db 5701 ATTTTCAACCTGAAACCGTGCACCTAGTAGAACCTCATTTTAAAGATTTAAACACAGGA 5760
Qy
|||||
Db 5761 AATAAATTTGTAAGAAAGGTTTCT 5784
Qy
|||||
Db 5761 AATAAATTTGTAAGAAAGGTTTCT 5784
```

RESULT 2

ABK10277

ID ABK10277 standard; cDNA; 5784 BP.

XX ABK10277;

XX ABK10277;

XX 21-MAY-2002 (first entry)

XX Human cDNA encoding thrombospondin 2 protein.

XX DE

XX DE

XX KW

KW Human; Osteopontin 1; OPN1; ss; gene; thrombospondin 2;

KW wound response; foreign body response; cut; abrasion; burn;

KW vulnerable.

XX KW

XX OS

XX Homo sapiens.

XX FH

FH Key

CDS Location/Qualifiers

FT 240..3758

FT /*tag= a

FT /product= "Thrombospondin 2 protein"

XX PN

WO200209735-A2.

QY 1561 GCCACTGGTCACTTGGTCTTTCATGCTCTGTGACCTGTGGAGTTGGCAATATACACAGCA 1620
DB 1561 GCCACTGGTCACTTGGTCTTTCATGCTCTGTGACCTGTGGAGTTGGCAATATACACAGCA 1620
QY 1621 TCCGCTCTCTGCAACTCCCCAGTGCACAGATGGGGGCAAGAAATGCAAGAGGAGTGCC 1680
DB 1621 TCCGCTCTCTGCAACTCCCCAGTGCACAGATGGGGGCAAGAAATGCAAGAGGAGTGCC 1680
QY 1681 GGGAGACCAAAAGCTGCCAGGGGCCCATGCCCCAATCATGATGCCGCTGGAGCCCTGTGT 1740
DB 1681 GGGAGACCAAAAGCTGCCAGGGGCCCATGCCCCAATCATGATGCCGCTGGAGCCCTGTGT 1740
QY 1741 CCCGCTGTGGCCTGTGCACTGTCACTGTGCGCGTGGGATCGGGAGCGCACCCGGGTCT 1800
DB 1741 CCCGCTGTGGCCTGTGCACTGTCACTGTGCGCGTGGGATCGGGAGCGCACCCGGGTCT 1800
QY 1801 GCAACAGCCCTCAGCCTCAGTACGAGGGAAGCCCTGCTGGGGGATGTGCAGGAGCGTC 1860
DB 1801 GCAACAGCCCTCAGCCTCAGTACGAGGGAAGCCCTGCTGGGGGATGTGCAGGAGCGTC 1860
QY 1861 AGATGTGCAACAAAGAGGAGTGCCTCGTGGATGGCTGTTTATCCAAACCCCTGCTTCCCGG 1920
DB 1861 AGATGTGCAACAAAGAGGAGTGCCTCGTGGATGGCTGTTTATCCAAACCCCTGCTTCCCGG 1920
QY 1921 GAGCCAGTGCAGAGCTTCCCGATGGGTCTGTGTCATGCGGCTTGTGCGCTGTGGGT 1980
DB 1921 GAGCCAGTGCAGAGCTTCCCGATGGGTCTGTGTCATGCGGCTTGTGCGCTGTGGGT 1980
QY 1981 TCTTGGGCAATGGCAACCACTGTGAGGACCTGGAGAGTGTGCCCTGCTGCCCGACATCT 2040
DB 1981 TCTTGGGCAATGGCAACCACTGTGAGGACCTGGAGAGTGTGCCCTGCTGCCCGACATCT 2040
QY 2041 GCTTCTCCACCAAGAGTGCCTGCTGTGCAACACTCAGCCTGCTTCCACTGCCCTGC 2100
DB 2041 GCTTCTCCACCAAGAGTGCCTGCTGTGCAACACTCAGCCTGCTTCCACTGCCCTGC 2100
QY 2101 CCGTCCCGCCGATACAGAGGAACACGCGCTGGGGTGGCCCTGGAAGAGCCCAAGA 2160
DB 2101 CCGTCCCGCCGATACAGAGGAACACGCGCTGGGGTGGCCCTGGAAGAGCCCAAGA 2160
QY 2161 CGGAAAGCAAGTGTGAGCCCGCAAAACCCATGCAAGGACACACACTGCCACA 2220
DB 2161 CGGAAAGCAAGTGTGAGCCCGCAAAACCCATGCAAGGACACACACTGCCACA 2220
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DB 2221 AGCAGCGGAGTGCATCTACCTGGTCACTTCAGCGACCCCATGTGTAAGTGCAGTGCC 2280
QY 2281 AGCAGGCTACGCGGGCAGCGGCTCATCTGCGGGAGAGTTCGGACCTGGACGGCTGGC 2340
DB 2281 AGCAGGCTACGCGGGCAGCGGCTCATCTGCGGGAGAGTTCGGACCTGGACGGCTGGC 2340
QY 2341 CCAACCTCAATCTGTCTGCGCCACCAAGCCACTTACCTGCAATCAAGTAACTGCC 2400
DB 2341 CCAACCTCAATCTGTCTGCGCCACCAAGCCACTTACCTGCAATCAAGTAACTGCC 2400
QY 2401 CCCATCTGCCAAATCTGGGAGGAAGACTTTGACAAGGACGGGATTTGGCGATGCCCTGTG 2460
DB 2401 CCCATCTGCCAAATCTGGGAGGAAGACTTTGACAAGGACGGGATTTGGCGATGCCCTGTG 2460
QY 2461 ATGATGACGATGACAAATGACCGTGTGACCGATGAGAGGACAATGCCAGCTCCTTTCA 2520
DB 2461 ATGATGACGATGACAAATGACCGTGTGACCGATGAGAGGACAATGCCAGCTCCTTTCA 2520
QY 2521 ATCCCGCCAGGCTGACTATGACAGGATGAGTTGGGACCGCTGTGACAACTGCCCTT 2580
DB 2521 ATCCCGCCAGGCTGACTATGACAGGATGAGTTGGGACCGCTGTGACAACTGCCCTT 2580
QY 2581 ACGTGCACAAACCTGCCAGATCGACACAGACAACAAATGGAGGGTGACGCTGCTCCG 2640
DB 2581 ACGTGCACAAACCTGCCAGATCGACACAGACAACAAATGGAGGGTGACGCTGCTCCG 2640

QY 2641 TGGACATTTGATGGGACGATGCTTCAATGAACGAGACAATTTGTCCTTACGCTTACAACA 2700
DB 2641 TGGACATTTGATGGGACGATGCTTCAATGAACGAGACAATTTGTCCTTACGCTTACAACA 2700
QY 2701 CTGACACAGAGGACACGGATGCTGAGCGTGTGGGATCAGTGTGACACTGCCCCCTGG 2760
DB 2701 CTGACACAGAGGACACGGATGCTGAGCGTGTGGGATCAGTGTGACACTGCCCCCTGG 2760
QY 2761 TGCACAACCCCTCACCAGACCGACGTGGACAATGACTTGTGGGACCACTGTGACAACA 2820
DB 2761 TGCACAACCCCTCACCAGACCGACGTGGACAATGACTTGTGGGACCACTGTGACAACA 2820
QY 2821 ACGAGACATAGATGACGACGCCACCAAGACAACAGAGCAACTGCCCTACATCTCCA 2880
DB 2821 ACGAGACATAGATGACGACGCCACCAAGACAACAGAGCAACTGCCCTACATCTCCA 2880
QY 2881 AGCCCAACCCAGGCTGACCATGACAGACGGCCAGGGGACGCCCTGTGACCTGATGATG 2940
DB 2881 AGCCCAACCCAGGCTGACCATGACAGACGGCCAGGGGACGCCCTGTGACCTGATGATG 2940
QY 2941 ACAACGATGGGCTCCCGATGACAGGACAACCTGCCGGCTTGTTCACCCAGACACAGG 3000
DB 2941 ACAACGATGGGCTCCCGATGACAGGACAACCTGCCGGCTTGTTCACCCAGACACAGG 3000
QY 3001 AGGACTTGGACGGTGTGACGGGGTGATATTTGTAAGATGATTTTGACAATGACAACA 3060
DB 3001 AGGACTTGGACGGTGTGACGGGGTGATATTTGTAAGATGATTTTGACAATGACAACA 3060
QY 3061 TCCAGATATTGATGATGCTGCTGAAACAATGCCATCAGTGAGACAGACTTCAGGA 3120
DB 3061 TCCAGATATTGATGATGCTGCTGAAACAATGCCATCAGTGAGACAGACTTCAGGA 3120
QY 3121 ACTTCCAGATGGTCCCTTGGATCCAAAGGACCAACCAATTTGATCCCAACTGGGTCA 3180
DB 3121 ACTTCCAGATGGTCCCTTGGATCCAAAGGACCAACCAATTTGATCCCAACTGGGTCA 3180
QY 3181 TTCGCCATCAAGGCAAGGAGTGTTCAGACAGCAACTCGGACCCCGGCTATGCTGTAG 3240
DB 3181 TTCGCCATCAAGGCAAGGAGTGTTCAGACAGCAACTCGGACCCCGGCTATGCTGTAG 3240
QY 3241 GTTTTGGACGAGTTGGGTCTGTTGGTACCAGTCAAGCAGCGCTTCTATGTGGTGA 3300
DB 3241 GTTTTGGACGAGTTGGGTCTGTTGGTACCAGTCAAGCAGCGCTTCTATGTGGTGA 3300
QY 3301 ACGAGACTATGCTGGCTTCGTTGGTACCAGTCAAGCAGCGCTTCTATGTGGTGA 3360
DB 3301 ACGAGACTATGCTGGCTTCGTTGGTACCAGTCAAGCAGCGCTTCTATGTGGTGA 3360
QY 3361 TGTGGAAGCAGGTGACGAGACCTACTGGGAGGACCAACCCAGCGGGCTTATGGCTACT 3420
DB 3361 TGTGGAAGCAGGTGACGAGACCTACTGGGAGGACCAACCCAGCGGGCTTATGGCTACT 3420
QY 3421 CCGGCTGTCCCTCAAGTGTGAACTCCACCGGGACGGGACGACCTGAGGAACG 3480
DB 3421 CCGGCTGTCCCTCAAGTGTGAACTCCACCGGGACGGGACGACCTGAGGAACG 3480
QY 3481 CGCTGTGACACACGGGGAACACGCGGGGCAAGTTCGCAACCTTATGGCAGCAGCCAGGA 3540
DB 3481 CGCTGTGACACACGGGGAACACGCGGGGCAAGTTCGCAACCTTATGGCAGCAGCCAGGA 3540
QY 3541 ACATTTGGCTGAAGGACTTACACGGCCCTATAGGTGGCAGCTGACACAGGCCCCAAGACCG 3600
DB 3541 ACATTTGGCTGAAGGACTTACACGGCCCTATAGGTGGCAGCTGACACAGGCCCCAAGACCG 3600
QY 3601 GCTACATCAGAGTCTTAGTGATGAAGGAAACAGGTATGCGAGCTCAGGACCTATCT 3660
DB 3601 GCTACATCAGAGTCTTAGTGATGAAGGAAACAGGTATGCGAGCTCAGGACCTATCT 3660
QY 3661 ATGACCAAACTTACGCTGGCGGGGCTGCTTATTTGCTTCTCTCAAGAAATGGTCT 3720
DB 3661 ATGACCAAACTTACGCTGGCGGGGCTGCTTATTTGCTTCTCTCAAGAAATGGTCT 3720
QY 3721 ATTTCTCAGACCTCAAGTACGAATGCAGAGATATTTAAACAAGATTTGCTGCATTTCCGG 3780

[illegible]

Db	4801	ATTTTAAATATGCGCTAGTTAACACATATGTAGTATATAATTTCTAGAAACAAACATCTAATAA	4861
Qy	4861	GTATATAAATCCCTGTGAAAAATATGAGCGCTGTGATAATATTAGTGTGTCCAGATGAAGCATGC	4920
Db	4861	GTATATAAATCCCTGTGAAAAATATGAGCGCTGTGATAATATTAGTGTGTCCAGATGAAGCATGC	4920
Qy	4921	TAGAAGCTGTACACAGAAATACATAGAGAAATAATGAGGAGTTTATGATGGAAACCTTTAATATA	4980
Db	4921	TAGAAGCTGTACACAGAAATACATAGAGAAATAATGAGGAGTTTATGATGGAAACCTTTAATATA	4980
Qy	4981	TAATGTTGCCAGCGATTTTAGTTCATATTTGTTACTGTTACTCTATCTCTGCTGCTATATGGA	5040
Db	4981	TAATGTTGCCAGCGATTTTAGTTCATATTTGTTACTGTTACTCTATCTCTGCTGCTATATGGA	5040
Qy	5041	ATTCTTTTAATTCAAACGCTGAAAACGAATCAGCATTTAGTCTGTGCCAGGCACACCCCAAT	5100
Db	5041	ATTCTTTTAATTCAAACGCTGAAAACGAATCAGCATTTAGTCTGTGCCAGGCACACCCCAAT	5100
Qy	5101	AATCAGTCATGTGTAATATGCAACAAGTTGTTTGTGTTTGTGTTTGTGTTTGTGTTGGTGGT	5160
Db	5101	AATCAGTCATGTGTAATATGCAACAAGTTGTTTGTGTTTGTGTTTGTGTTTGTGTTGGTGGT	5160
Qy	5161	TTTTTGTGCTTTAAGTTGTCATGATCTTTCTGCAGGAATAAGTCACTATCCCACTCCCAAT	5220
Db	5161	TTTTTGTGCTTTAAGTTGTCATGATCTTTCTGCAGGAATAAGTCACTATCCCACTCCCAAT	5220
Qy	5221	AAGGGGTTTAGTAAGAGAAGTCTGCTGCTGATGATGGATAGGGGCAAACTCTTTTCC	5280
Db	5221	AAGGGGTTTAGTAAGAGAAGTCTGCTGCTGATGATGGATAGGGGCAAACTCTTTTCC	5280
Qy	5281	CCTTCTCTGTTAATAGTCAATCACAATTTCTATGCCAAACAGGAAGCATCCATAACTTTAGTC	5340
Db	5281	CCTTCTCTGTTAATAGTCAATCACAATTTCTATGCCAAACAGGAAGCATCCATAACTTTAGTC	5340
Qy	5341	TTAATGTCACATATGCATTTTGTATAAATTAATTTTGTGTTTCCCTTGAGGTTGATCGT	5400
Db	5341	TTAATGTCACATATGCATTTTGTATAAATTAATTTTGTGTTTCCCTTGAGGTTGATCGT	5400
Qy	5401	TGTGTTGTTTGTGTCGACATTTTACATTTTGTGCTGAGAGCTGATTCGCCGAGACAACG	5460
Db	5401	TGTGTTGTTTGTGTCGACATTTTACATTTTGTGCTGAGAGCTGATTCGCCGAGACAACG	5460
Qy	5461	AAGCGTTGGGATACATTCATTAATATGAGCAGCTGTCAACAGCGTCGAGGTTTCTGTTTC	5520
Db	5461	AAGCGTTGGGATACATTCATTAATATGAGCAGCTGTCAACAGCGTCGAGGTTTCTGTTTC	5520
Qy	5521	TGTGTTGTCGGGTCAACCGTACAAATGGTGTGGGAATGACGATGATGTAATATTTAGAAT	5580
Db	5521	TGTGTTGTCGGGTCAACCGTACAAATGGTGTGGGAATGACGATGATGTAATATTTAGAAT	5580
Qy	5581	GTACCATATTTTGTGTAATATTTATGTTTCTTAACAAATTTATCGTATAGGTTGAT	5640
Db	5581	GTACCATATTTTGTGTAATATTTATGTTTCTTAACAAATTTATCGTATAGGTTGAT	5640
Qy	5641	GAAACGTCATGTGTTTGTGCCAAGACGTGTAATATTTATGTTCTACATGTTCAACAA	5700
Db	5641	GAAACGTCATGTGTTTGTGCCAAGACGTGTAATATTTATGTTCTACATGTTCAACAA	5700
Qy	5701	ATTTCACCACTGAAACCCCTGCACTTAGCTAGAACCTCAATTTTTAAAGATTAAACAACAGGA	5760
Db	5701	ATTTCACCACTGAAACCCCTGCACTTAGCTAGAACCTCAATTTTTAAAGATTAAACAACAGGA	5760
Qy	5761	ATAAATTCGTAAAAAGGTTTCT	5784
Db	5761	ATAAATTCGTAAAAAGGTTTCT	5784

DT	15-MAY-2002	(first entry)
XX		
DE	Colon adenocarcinoma related gene sequence SEQ ID NO:997.	
XX		
KW	Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;	
KW	stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;	
KW	cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;	
KW	gene; ds.	
XX		
OS	Homo sapiens.	
OS		
XX		
PN	WO200194629-A2.	
PN		
XX		
PD	13-DEC-2001.	
XX		
PF	30-MAY-2001; 2001WO-US10838.	
PF		
XX	05-JUN-2000; 2000US-209473P.	
XX	05-JUN-2000; 2000US-209531P.	
PR	18-SEP-2000; 2000US-233133P.	
PR	18-SEP-2000; 2000US-233617P.	
PR	20-SEP-2000; 2000US-234009P.	
PR	20-SEP-2000; 2000US-234034P.	
PR	20-SEP-2000; 2000US-234052P.	
PR	22-SEP-2000; 2000US-234509P.	
PR	22-SEP-2000; 2000US-234567P.	
PR	25-SEP-2000; 2000US-234923P.	
PR	25-SEP-2000; 2000US-234924P.	
PR	25-SEP-2000; 2000US-235077P.	
PR	25-SEP-2000; 2000US-235082P.	
PR	25-SEP-2000; 2000US-235134P.	
PR	25-SEP-2000; 2000US-235280P.	
PR	26-SEP-2000; 2000US-235637P.	
PR	26-SEP-2000; 2000US-235638P.	
PR	27-SEP-2000; 2000US-235711P.	
PR	27-SEP-2000; 2000US-235720P.	
PR	27-SEP-2000; 2000US-235840P.	
PR	27-SEP-2000; 2000US-235863P.	
PR	28-SEP-2000; 2000US-236028P.	
PR	28-SEP-2000; 2000US-236032P.	
PR	28-SEP-2000; 2000US-236033P.	
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PR	28-SEP-2000; 2000US-236109P.	
PR	28-SEP-2000; 2000US-236111P.	
PR	29-SEP-2000; 2000US-236842P.	
PR	29-SEP-2000; 2000US-236891P.	
PR	02-OCT-2000; 2000US-237172P.	
PR	02-OCT-2000; 2000US-237173P.	
PR	02-OCT-2000; 2000US-237278P.	
PR	02-OCT-2000; 2000US-237294P.	
PR	02-OCT-2000; 2000US-237295P.	
PR	02-OCT-2000; 2000US-237316P.	
PR	03-OCT-2000; 2000US-237425P.	
PR	03-OCT-2000; 2000US-237598P.	
PR	03-OCT-2000; 2000US-237604P.	
PR	03-OCT-2000; 2000US-237606P.	
PR	03-OCT-2000; 2000US-237608P.	
PR	01-NOV-2000; 2000US-244867P.	
PR	01-NOV-2000; 2000US-245084P.	
XX		
PA	(AVAL-) AVALON PHARM.	
PA		
XX	Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;	
PI	Soppet DR, Weaver Z;	
PI		
XX	WPI; 2002-188264/24.	
XX		
PT	Screening for anti-neoplastic agent involves exposing cells to a	
PT	chemical agent to be tested for anti-neoplastic activity, and	
PT	determining a change in expression of a gene of a signature gene set	
XX	Claim 1; SEQ ID 997; 44pp; English.	
XX		

|||||
Db 721 ACAGCTTGCAGTGGGTGGACCTCATAGGACCAGTTGCTCTGGACGAGCCCTCTACG 780
QY 781 AGCACCTGCGAGGGGAAAAGAGCGGATGTACGTGGCCAAAGGCTCTGCCAGAGAGATC 840
Db 781 AGCACCTGCGAGGGGAAAAGAGCGGATGTACGTGGCCAAAGGCTCTGCCAGAGAGATC 840
QY 841 ACTTCAGGGTTGCTTCAGAACGTCACCTAGTGTGTTGAAAACCTCTGTGGAAGATATTC 900
Db 841 ACTTCAGGGTTGCTTCAGAACGTCACCTAGTGTGTTGAAAACCTCTGTGGAAGATATTC 900
QY 901 TAAGCAAGAAGGTTGCGACGAAGCGGACGAGCTGAGATCAACGCCATCAGTCAGAACCA 960
Db 901 TAAGCAAGAAGGTTGCGACGAAGCGGACGAGCTGAGATCAACGCCATCAGTCAGAACCA 960
QY 961 CAGAGACGCTGCGGCTCGGCTCCGATGTCAACACCGAGTACGTGGGCCCCAGCTCGGAGA 1020
Db 961 CAGAGACGCTGCGGCTCGGCTCCGATGTCAACACCGAGTACGTGGGCCCCAGCTCGGAGA 1020
QY 1021 GGAGGCCGAGGTTGCGAAGCTCGTCGAGGAGCTGGGAACATGTTCCAGGAGCTCT 1080
Db 1021 GGAGGCCGAGGTTGCGAAGCTCGTCGAGGAGCTGGGAACATGTTCCAGGAGCTCT 1080
QY 1081 CGGGGCTCCAGCTCGTCTGAACAGCTCAGCGAGAACCCTCAAGAGAGTGTGGAATGATA 1140
Db 1081 CGGGGCTCCAGCTCGTCTGAACAGCTCAGCGAGAACCCTCAAGAGAGTGTGGAATGATA 1140
QY 1141 ACCAGTTTCTCTGGAGCTCATTTGGTGGCCCTCCTTAAGAACGAAGAACTGTACGCTTGCT 1200
Db 1141 ACCAGTTTCTCTGGAGCTCATTTGGTGGCCCTCCTTAAGAACGAAGAACTGTACGCTTGCT 1200
QY 1201 GGCAGGATGCGCGTTCTTTGCGGAAAATGAACGTTGGTGGAGCTGCACACAGT 1260
Db 1201 GGCAGGATGCGCGTTCTTTGCGGAAAATGAACGTTGGTGGAGCTGCACACAGT 1260
QY 1261 GTACCTGCAAGAAATTTAAACCAATTTGCCACAAATCACTGCCCGCTGCAACCTGCG 1320
Db 1261 GTACCTGCAAGAAATTTAAACCAATTTGCCACAAATCACTGCCCGCTGCAACCTGCG 1320
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Db 1321 CCAGTCCATCCTTTGTGGAAGGGAATGCTGCCCTTCTGCTCCACTCGGTGGACGGTG 1380
QY 1381 AGGAGGCTGGTCTCCGTGGGACAGTGGACCAAGTGCCTGGTACAGTGTGGCTCTGGGA 1440
Db 1381 AGGAGGCTGGTCTCCGTGGGACAGTGGACCAAGTGCCTGGTACAGTGTGGCTCTGGGA 1440
QY 1441 CCCAGCAGAGAGCGGCTCTGTGACGTCAACAGCAACCTGCTGGGGCCCTCGATCC 1500
Db 1441 CCCAGCAGAGAGCGGCTCTGTGACGTCAACAGCAACCTGCTGGGGCCCTCGATCC 1500
QY 1501 AGACACGGGCTTGCAAGTGTGAGCAAGTGTGACACCCGATCCGGCAGGACGGCGGCTGGA 1560
Db 1501 AGACACGGGCTTGCAAGTGTGAGCAAGTGTGACACCCGATCCGGCAGGACGGCGGCTGGA 1560
QY 1561 GCCACTGGTACCTTGTCTGTATGCTGTGACCTGTGACCTGCTGGGGCCCTCGATCC 1620
Db 1561 GCCACTGGTACCTTGTCTGTATGCTGTGACCTGTGACCTGCTGGGGCCCTCGATCC 1620
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Db 1621 TCCGTCTCTGCAACTCCCGAGTGGCCAGATGGGGGCAAGAAATTGCAAGGGAGTGGCC 1680
QY 1681 GGGAGACCAAGCTGCCAGGGGCCCCATGCCAAATCGATGGCCGCTGGAGCCCTGGT 1740
Db 1681 GGGAGACCAAGCTGCCAGGGGCCCCATGCCAAATCGATGGCCGCTGGAGCCCTGGT 1740
QY 1741 CCGGCTGGTGGCTGTCACTGTACCTGTGCGGTTGGATCCGGGACGCAACCGGGTCT 1800
Db 1741 CCGGCTGGTGGCTGTCACTGTGCGGTTGGATCCGGGACGCAACCGGGTCT 1800
QY 1801 GCAACGCCCTGAGCCTCAGTACGAGGGAAGGCTCGTGGGGATGTGCAGGAGGCTC 1860
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Db 1801 GCAACGCCCTGAGCCTCAGTACGAGGGAAGGCTCGTGGGGGATGTGCAGGAGGCTC 1860
QY 1861 AGATGTGCAACAAGAGGAGCTGCCCCGTGGATGCTGTTTATCAACCCCTGCTTCCCGG 1920
Db 1861 AGATGTGCAACAAGAGGAGCTGCCCCGTGGATGCTGTTTATCAACCCCTGCTTCCCGG 1920
QY 1921 GAGCCAGTGCAGCAGCTTCCCCGATGGTCTGATCGGGCTTCTGCCCTTGGGCT 1980
Db 1921 GAGCCAGTGCAGCAGCTTCCCCGATGGTCTGATCGGGCTTCTGCCCTTGGGCT 1980
QY 1981 TCTTGGCAATGGCACCACCTGTGAGGACCTGGAGAGTGGCCCTGTGTCCCCGACATCT 2040
Db 1981 TCTTGGCAATGGCACCACCTGTGAGGACCTGGAGAGTGGCCCTGTGTCCCCGACATCT 2040
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Db 2041 GCTTCTCCACCAGCAAGTGCCTCGCTGTGTCAACACTCAGCCTGGCTTCCACTGCCCTG 2100
QY 2101 CCTGCCCGCCCCGATACAGAGGAACAGCCGTCGGGGTGGCTTGGGAAGCAGCCAGA 2160
Db 2101 CCTGCCCGCCCCGATACAGAGGAACAGCCGTCGGGGTGGCTTGGGAAGCAGCCAGA 2160
QY 2161 CGGAAAAGCAAGTGTGTGAGCCCGAAAACCCATCAAGGACAAAGACACAACTGCCACA 2220
Db 2161 CGGAAAAGCAAGTGTGTGAGCCCGAAAACCCATCAAGGACAAAGACACAACTGCCACA 2220
QY 2221 AGCAGCGGAGTGCATCTACCTGGTCACTTTCAGCGACCCCATGTACAAGTGGAGTGGC 2280
Db 2221 AGCAGCGGAGTGCATCTACCTGGTCACTTTCAGCGACCCCATGTACAAGTGGAGTGGC 2280
QY 2281 AGCAGGCTAGCGGGGACGGGCTCATCTCGGGGGAGGACTCGGACCTGACGGCTGGC 2340
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QY 2341 CCAACCTCAATCTGCTGCGCCACCAAGGCCACTTACCTGATCAAGGATAACTGCC 2400
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QY 2401 CCCATCTGCCAAATTTCTGGGCGAGGAAGACTTTGACAGGACGGGATGGCGATGCCGTG 2460
Db 2401 CCCATCTGCCAAATTTCTGGGCGAGGAAGACTTTGACAGGACGGGATGGCGATGCCGTG 2460
QY 2461 ATGATGAGGATGACAATGACGGTGTGACCGATGAGAGGACAACCTGCCAGCTCTCTTCA 2520
Db 2461 ATGATGAGGATGACAATGACGGTGTGACCGATGAGAGGACAACCTGCCAGCTCTCTTCA 2520
QY 2521 ATCCCCCGCAGGCTGACTATGACAAGGATGAGTTGGGACCGCTGTGACAACCTGCCCT 2580
Db 2521 ATCCCCCGCAGGCTGACTATGACAAGGATGAGTTGGGACCGCTGTGACAACCTGCCCT 2580
QY 2581 ACGTGCAACAACCTTGCCCAGATCGACACAGACAATGGAGGGTGAACGCTGCTCCG 2640
Db 2581 ACGTGCAACAACCTTGCCCAGATCGACACAGACAATGGAGGGTGAACGCTGCTCCG 2640
QY 2641 TGGACATTGATGGGACGATGCTCTCAATGAACGAGACAATTTGCCCTACGCTCTACAACA 2700
Db 2641 TGGACATTGATGGGACGATGCTCTCAATGAACGAGACAATTTGCCCTACGCTCTACAACA 2700
QY 2701 CTGACACAGAGGACACGGATGCTGACGGTGTGGGGATCACTGTGACAACCTGCCCTGG 2760
Db 2701 CTGACACAGAGGACACGGATGCTGACGGTGTGGGGATCACTGTGACAACCTGCCCTGG 2760
QY 2761 TGCACAACCTTGACCAGACCGCTGACAAATGACCTTTGTTGGGGACAGTGTGACAACA 2820
Db 2761 TGCACAACCTTGACCAGACCGCTGACAAATGACCTTTGTTGGGGACAGTGTGACAACA 2820
QY 2821 ACGAGGACATAGATGACGACGGCCACAGAACACAGGACAACCTGCCCTTACATCTCCA 2880
Db 2821 ACGAGGACATAGATGACGACGGCCACAGAACACAGGACAACCTGCCCTTACATCTCCA 2880
QY 2881 ACGCCAACCGGCTGACCATGACAGACGCGGCGGCTGTGACCCCTGATGATG 2940
Db 2881 ACGCCAACCGGCTGACCATGACAGACGCGGCGGCTGTGACCCCTGATGATG 2940

QY 2941 ACAACGATGGCTCCCGGATGACAGGGAACAATGCCGGCTTGTTCAACCCAGACCAGG 3000
DB 2941 ACAACGATGGCTCCCGGATGACAGGGAACAATGCCGGCTTGTTCAACCCAGACCAGG 3000
QY 3001 AGGACATTGGACGGTGATGACGGGGTGATATTGTAAAGATGATTTGACAAATGACAA 3060
DB 3001 AGGACATTGGACGGTGATGACGGGGTGATATTGTAAAGATGATTTGACAAATGACAA 3060
QY 3061 TCCAGATATTGATGATGTGTCTCTGAAACAAATGCCATCAGTGAGACAGACTTCAGGA 3120
DB 3061 TCCAGATATTGATGATGTGTCTCTGAAACAAATGCCATCAGTGAGACAGACTTCAGGA 3120
QY 3121 ACTTCAGATGGTCCCTTTGGATCCCAAGAGGACCAACCAATATGATCCCAACTGGGTCA 3180
DB 3121 ACTTCAGATGGTCCCTTTGGATCCCAAGAGGACCAACCAATATGATCCCAACTGGGTCA 3180
QY 3181 TTCGCCATCAAGCAAGGAGCTGGTTTCACACAGCCAACTCGACCCCGCATCGCTGTAG 3240
DB 3181 TTCGCCATCAAGCAAGGAGCTGGTTTCACACAGCCAACTCGACCCCGCATCGCTGTAG 3240
QY 3241 GTTTTGACGAGTTGGGCTCTGAGACTTCAGTGGCACATTCCTACGTAAACACTGACCGGG 3300
DB 3241 GTTTTGACGAGTTGGGCTCTGAGACTTCAGTGGCACATTCCTACGTAAACACTGACCGGG 3300
QY 3301 AGCAGACTATGCTGGCTTCGTTTGGTTACAGTCAAGCAGCCGCTTCTATGTGGTGA 3360
DB 3301 AGCAGACTATGCTGGCTTCGTTTGGTTACAGTCAAGCAGCCGCTTCTATGTGGTGA 3360
QY 3361 TGTGAAGCAGTGCAGCAGACCTACTGGAGGAGCAGCCAGCCAGCGGGCTATGCTACT 3420
DB 3361 TGTGAAGCAGTGCAGCAGACCTACTGGAGGAGCAGCCAGCCAGCGGGCTATGCTACT 3420
QY 3421 CCGCGGTGTCCTCAAGTGGTGAATCCACACGCGGACGCGGACGACCTTGAGGAAG 3480
DB 3421 CCGCGGTGTCCTCAAGTGGTGAATCCACACGCGGACGCGGACGACCTTGAGGAAG 3480
QY 3481 CCCTGTGGACAGCGGGAACACCGCGGGCAGGTGCGAACCCTTATGGCAGACCCAGGA 3540
DB 3481 CCCTGTGGACAGCGGGAACACCGCGGGCAGGTGCGAACCCTTATGGCAGACCCAGGA 3540
QY 3541 ACATTGGCTGGAAGACTACAGCGCTATAGTGGCAGCTGACTCACAGGCCCAAGACCG 3600
DB 3541 ACATTGGCTGGAAGACTACAGCGCTATAGTGGCAGCTGACTCACAGGCCCAAGACCG 3600
QY 3601 GCTACATCAGACTCTTAGTGCATGAAGGAAACAGGTGATGCGACACTCAGGACCTATCT 3660
DB 3601 GCTACATCAGACTCTTAGTGCATGAAGGAAACAGGTGATGCGACACTCAGGACCTATCT 3660
QY 3661 ATGACCAAACTACGCTGGCGGGCGCTGGGTCTATTGTCCTCTCAAGAAATGGTCT 3720
DB 3661 ATGACCAAACTACGCTGGCGGGCGCTGGGTCTATTGTCCTCTCAAGAAATGGTCT 3720
QY 3721 ATTTTCTCAGACCTCAAGTACGAATGCAGAGATATTTAAACAGATTTGCTGCATTTCCGG 3780
DB 3721 ATTTTCTCAGACCTCAAGTACGAATGCAGAGATATTTAAACAGATTTGCTGCATTTCCGG 3780
QY 3781 CAATGCCCTGTGCATGCCATGGTCCCTAGACACCTCAGTTCATTTGCTGCTTGGCGCT 3840
DB 3781 CAATGCCCTGTGCATGCCATGGTCCCTAGACACCTCAGTTCATTTGCTGCTTGGCGCT 3840
QY 3841 CTCCTCTAGCAGACCTCCCTGTCCTTGAACCTTAACCTGATGCTGATGCTTCACTCCG 3900
DB 3841 CTCCTCTAGCAGACCTCCCTGTCCTTGAACCTTAACCTGATGCTGATGCTTCACTCCG 3900
QY 3901 CAGCAACCCCAACCAAGTGCCTTCAGAGGATAAATATCAATGAACCTCAGAGATGAAC 3960
DB 3901 CAGCAACCCCAACCAAGTGCCTTCAGAGGATAAATATCAATGAACCTCAGAGATGAAC 3960
QY 3961 ATCTAACCCACTTAGAGAAACAGTTTGGTGATATATGAGACTTTATGTGGAGTGAATA 4020
DB 3961 ATCTAACCCACTTAGAGAAACAGTTTGGTGATATATGAGACTTTATGTGGAGTGAATA 4020

QY 4021 TGGGATGCCATTACATGCTTTTTCTTGTGTTTAAAGAAATGACGCTTTACATATAA 4080
DB 4021 TGGGATGCCATTACATGCTTTTTCTTGTGTTTAAAGAAATGACGCTTTACATATAA 4080
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DB 4081 AATGTAATTTACTTATTGTATTTATGTTATATGGAGTTCAAGGGAATCTGTGCAATAGC 4140
QY 4141 CATTATGATAAATTAAGCATGAAAAATATGCTGAACCTACTTTTGTGCTTAAAGTTGTC 4200
DB 4141 CATTATGATAAATTAAGCATGAAAAATATGCTGAACCTACTTTTGTGCTTAAAGTTGTC 4200
QY 4201 ACTATTTCTTGAATTTAGAGTTGCTCTACAAATGACACACAAATCCCGCTAAATATAA 4260
DB 4201 ACTATTTCTTGAATTTAGAGTTGCTCTACAAATGACACACAAATCCCGCTAAATATAA 4260
QY 4261 ACAAGGTCAAATTTCAAAATTTAGTAAATTTAGTAAAGGAGAGATTAGAAGCAACAGG 4320
DB 4261 ACAAGGTCAAATTTCAAAATTTAGTAAATTTAGTAAAGGAGAGATTAGAAGCAACAGG 4320
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DB 4321 CATAGCAATGACATAAGCTACCGATTAACTAATCGGAACATGTAACACAGTTACAAAA 4380
QY 4381 TAAACGAACTCTCCCTCTGCTTCTACAAATGAAGCCCTCATGTGCAGTAGAGATGCACTT 4440
DB 4381 TAAACGAACTCTCCCTCTGCTTCTACAAATGAAGCCCTCATGTGCAGTAGAGATGCACTT 4440
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DB 4441 CATCAAGAACAAACATCCTTGCAAAATGGGTGAGCGGTTCCAGATGTGGATTGGCA 4500
QY 4501 AAACCTCATTTTAAAGTAAAGTTAGCAGAGCAAAAGTGGCGTCTTATAGTCTGCTTGTG 4560
DB 4501 AAACCTCATTTTAAAGTAAAGTTAGCAGAGCAAAAGTGGCGTCTTATAGTCTGCTTGTG 4560
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DB 4561 CCGTGTGGCGTGGGGAGGCTCTGCTGAGCTTCCCTTCCCGCAGCTTTGCTGCTGAGA 4620
QY 4621 GGAACGACAGACGACGACGAGCCGGAAGGCGCATCTAACGCGTATCTAGGCTTTGGT 4680
DB 4621 GGAACGACAGACGACGACGAGCCGGAAGGCGCATCTAACGCGTATCTAGGCTTTGGT 4680
QY 4681 AACTCGGACAAAGTTGCTTTTACCTGATTGATGATACATTTCAATTAAGTTCCAGTTAT 4740
DB 4681 AACTCGGACAAAGTTGCTTTTACCTGATTGATGATACATTTCAATTAAGTTCCAGTTAT 4740
QY 4741 AAATATTTTGTAAATATTATTAAAGTACTATAGTAATGCAACTCCATTTACGAGTAACCT 4800
DB 4741 AAATATTTTGTAAATATTATTAAAGTACTATAGTAATGCAACTCCATTTACGAGTAACCT 4800
QY 4801 ATTTTAAATATGCTGAAATATGAGGCTTGATAATATTAGGTGTCAGATGAAGCATGC 4860
DB 4801 ATTTTAAATATGCTGAAATATGAGGCTTGATAATATTAGGTGTCAGATGAAGCATGC 4860
QY 4861 GTATATAATGCTGAAATATGAGGCTTGATAATATTAGGTGTCAGATGAAGCATGC 4920
DB 4861 GTATATAATGCTGAAATATGAGGCTTGATAATATTAGGTGTCAGATGAAGCATGC 4920
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DB 4921 TAGAAGCTGTAAACAGATACATAGAGATAATAGGAGTTTATGATGAGAACTTAAATATA 4980
QY 4981 TAAATGTTCCAGGCACTTTAGTTTCAATATTGTTTACTCTTATCTATCTGCTGATATGGA 5040
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QY 5041 ATTTCTTTTAAATCAACGCTGAAAAACGAATCAGCATTTAGTCTTCCAGGACACCCCAAT 5100
DB 5041 ATTTCTTTTAAATCAACGCTGAAAAACGAATCAGCATTTAGTCTTCCAGGACACCCCAAT 5100
QY 5101 AATCAGTCACTGTAAATATGCAACAAAGTTGTTTGTGTTTTGTTTGTGTTGGTGGT 5160

QY 2471 TGACAAATGACGGGTGTGACCGATGAGAGGAGCAACTGCCAGCTCCTCTTCAATCCCGGCCA 2530
DB 454 TGACAAATGACGGGTGTGACCGATGAGAGGAGCAACTGCCAGCTCCTCTTCAATCCCGGCCA 513
QY 2531 GGGTGACTATGACAAAGATGAGGTTGGGACCGCTGTGACAACTGCCCTTACGTGCACAA 2590
DB 514 GGGTGACTATGACAAAGATGAGGTTGGGACCGCTGTGACAACTGCCCTTACGTGCACAA 573
QY 2591 CCTGCCAGATGACACACAGACAACAAATGAGAGGGTGACGGCTGTCTCGTGACATTGA 2650
DB 574 CCTGCCAGATGACACACAGACAACAAATGAGAGGGTGACGGCTGTCTCGTGACATTGA 633
QY 2651 TGGGGACGATGCTTCAATGAACGAGACAATTTGCCCTACGCTTACAACACTGACCAGAG 2710
DB 634 TGGGGACGATGCTTCAATGAACGAGACAATTTGCCCTACGCTTACAACACTGACCAGAG 693
QY 2711 GGACACGGATGTGACGGGTGGGGGATCACTGTGACAACTGCCCTGGTGACAAACCC 2770
DB 694 GGACACGGATGTGACGGGTGGGGGATCACTGTGACAACTGCCCTGGTGACAAACCC 753
QY 2771 TGACCAGACCGCGTGGACAAATGACCTTGTGGGACCAAGTGTGACAAACAGGACAT 2830
DB 754 TGACCAGACCGCGTGGACAAATGACCTTGTGGGACCAAGTGTGACAAACAGGACAT 813
QY 2831 AGATGACGACGGCCACAGACAACACAGGACAACCTGCCCTACATCTCCAACGCCAACCA 2890
DB 814 AGATGACGACGGCCACAGACAACACAGGACAACCTGCCCTACATCTCCAACGCCAACCA 873
QY 2891 GGCTGACCATGACAGAGACGGCCAGGGCGACCGCTGTGACCTGATGATGACAAAGATGG 2950
DB 874 GGCTGACCATGACAGAGACGGCCAGGGCGACCGCTGTGACCTGATGATGACAAAGATGG 933
QY 2951 CGTCCCGATGACAGGGACAACCTGCCGCTGTGTTCAACCCAGACAGGAGGACTTGA 3010
DB 934 CGTCCCGATGACAGGGACAACCTGCCGCTGTGTTCAACCCAGACAGGAGGACTTGA 993
QY 3011 CGGTGATGGACGGGTGATATTGTTAAAGATGATTTGACAATGACAACATCCAGATAT 3070
DB 994 CGGTGATGGACGGGTGATATTGTTAAAGATGATTTGACAATGACAACATCCAGATAT 1053
QY 3071 TCATGATGTGTCTCTGAAAACAAATGCCATCAGTCAGACAGACTTCAGGAATTCAGAT 3130
DB 1054 TCATGATGTGTCTCTGAAAACAAATGCCATCAGTCAGACAGACTTCAGGAATTCAGAT 1113
QY 3131 GGTCGCCCTTGGATCCCAAAGGACCAACCAAAATTTGATCCCACTGGGTCAATTCGCCATCA 3190
DB 1114 GGTCGCCCTTGGATCCCAAAGGACCAACCAAAATTTGATCCCACTGGGTCAATTCGCCATCA 1173
QY 3191 AGGCAAGGAGCTGGTTACAGACAGCCAACCTCGGACCCCGGCATFCGCTGTAGGTTTGA 3250
DB 1174 AGGCAAGGAGCTGGTTACAGACAGCCAACCTCGGACCCCGGCATFCGCTGTAGGTTTGA 1233
QY 3251 GTTTGGGCTGTGGACTTCAGTGGCACATTTACGTAAACACTGACGGGACGACGACTA 3310
DB 1234 GTTTGGGCTGTGGACTTCAGTGGCACATTTACGTAAACACTGACGGGACGACGACTA 1293
QY 3311 TGCTGGCTTCGCTTTGGTTACAGTCAAGACGCGCTTCTATGTGGTGATGTGGAAGCA 3370
DB 1294 TGCCGGCTTCGCTTTGGTTACAGTCAAGACGCGCTTCTATGTGGTGATGTGGAAGCA 1353
QY 3371 GGTGACGACGACCTACTGGGAGGACCAACCCACGCGGCCTATGGCTACTCCGGCGTGC 3430
DB 1354 GGTGACGACGACCTACTGGGAGGACCAACCCACGCGGCCTATGGCTACTCCGGCGTGC 1413
QY 3431 CCTCAAGTGTGTAATCCACACGGGACGGGCGAGACACCTGAGGAACGCGCTGTGCA 3490
DB 1414 CCTCAAGTGTGTAATCCACACGGGACGGGCGAGACACCTGAGGAACGCGCTGTGCA 1473
QY 3491 CACGGGGAACACGCGGGGACGAGTCCGAACCTTTATGGCACGACCCCGAGAACTTGGCTG 3550
DB 1474 CAGGGGAACACGCGGGGACGAGTCCGAACCTTTATGGCACGACCCCGAGAACTTGGCTG 1533

QY 3551 GAAGGACTACAGGGCCTATAGGTGGCACTAGTACAGGCCCCAAGACCGGTACATCAG 3610
DB 1534 GAAGGACTACAGGGCCTATAGGTGGCACTAGTACAGGCCCCAAGACTGGCTACATCAG 1593
QY 3611 AGTCTTAGTGCATGAGGAAAACAGGTCACTGGCAGACTCAGGACCTATCTATGACCAAC 3670
DB 1594 AGTCTTAGTGCATGAGGAAAACAGGTCACTGGCAGACTCAGGACCTATCTATGACCAAC 1653
QY 3671 CTACGCTGGCGGGCGCTGGGTCTATTTCTCTCTCAAGAAATGGTCTATTTCTCAGA 3730
DB 1654 CTACGCTGGCGGGCGCTGGGTCTATTTCTCTCTCAAGAAATGGTCTATTTCTCAGA 1713
QY 3731 CCTCAAGTACGAATCAGAGATATTTAAACAAGATTTGCTGCAATTTCCGGCAATGCCCTG 3790
DB 1714 CCTCAAGTACGAATCAGAGATATTTAAACAAGATTTGCTGCAATTTCCGGCAATGCCCTG 1773
QY 3791 TGCATGCCATGCTCCCTAGACACCTCAGTTCAATTTGGTCTCTTGGCTTCTCTCTTAG 3850
DB 1774 TGCATGCCATGCTCCCTAGACACCTCAGTTCAATTTGGTCTCTTGGCTTCTCTCTTAG 1833
QY 3851 CAGCACCTCCTGCTCCCTTGACCTTAACCTCTGATGGTTCTCACTCCTGCCAGCAACCCC 3910
DB 1834 CAGCACCTCCTGCTCCCTTGACCTTAACCTCTGATGGTTCTCACTCCTGCCAGCAACCCC 1893
QY 3911 AAACCCAAAGTGCCTTCAGAGGATAAATATCAATGGAACCTCAGAGATGAACATCTAACCCA 3970
DB 1894 AAACCCAAAGTGCCTTCAGAGGATAAATATCAATGGAACCTCAGAGATGAACATCTAACCCA 1953
QY 3971 CTAGAGGAACCCAGTTTGGTGATATGAGACTTTATGTGGAGTGAAATTTGGGATGCC 4030
DB 1954 CTAGAGGAACCCAGTTTGGTGATATGAGACTTTATGTGGAGTGAAATTTGGGATGCC 2013
QY 4031 ATTACATGCTTTTCTTTGTTTAAAAGAAGTACGCTTTACATATAAATGTAATTA 4090
DB 2014 ATTACATGCTTTTCTTTGTTTAAAAGAAGTACGCTTTACATATAAATGTAATTA 2073
QY 4091 CTATTGTTATTTATGTTATATGAGTTTGAAGGAATACTGTGCATTAAGCCATTTATGATA 4150
DB 2074 CTATTGTTATTTATGTTATATGAGTTTGAAGGAATACTGTGCATTAAGCCATTTATGATA 2133
QY 4151 AATTAAAGCATGAAAATATTTGCTGAACACTTTTGGTGGTTAAAGTTGTCACTATTCTTG 4210
DB 2134 AATTAAAGCATGAAAATATTTGCTGAACACTTTTGGTGGTTAAAGTTGTCACTATTCTTG 2193
QY 4211 AATTAGAGTTGCTCTACAATGACACACAAATCCCGCTAAATATAAACAAGGTCA 4270
DB 2194 AATTAGAGTTGCTCTACAATGACACACAAATCCCGCTAAATATAAACAAGGTCA 2253
QY 4271 AATTCAATTTGAAGTAATTTAGTAAGGAGAGATTAGAAGACAACAGGCATAGCAAT 4330
DB 2254 AATTCAATTTGAAGTAATTTAGTAAGGAGAGATTAGAAGACAACAGGCATAGCAAT 2313
QY 4331 GACATAAGCTACCGATTAACTAATCGGAACATGTAACAGTTTACAAAATAAACGAACT 4390
DB 2314 GACATAAGCTACCGATTAACTAATCGGAACATGTAACAGTTTACAAAATAAACGAACT 2373
QY 4391 CTCTCTTTGCTCTACAATGAAAGCCCTCATGTGCAAGTACAGTTTCAATCAAGAA 4450
DB 2374 CTCTCTTTGCTCTACAATGAAAGCCCTCATGTGCAAGTACAGTTTCAATCAAGAA 2433
QY 4451 CAACATCCTTTGCAATGGGTGTGACGGGTTCCAGATGTGGATTTGGCAAAACCTCATTT 4510
DB 2434 CAACATCCTTTGCAATGGGTGTGACGGGTTCCAGATGTGGATTTGGCAAAACCTCATTT 2493
QY 4511 TAAGTAAAGGTTAGCAGAGCAAGTGGGTGCTTTAGCTGCTGCTTGTGGGTTGTGGC 4570
DB 2494 TAAGTAAAGGTTAGCAGAGCAAGTGGGTGCTTTAGCTGCTGCTTGTGGGTTGTGGC 2553
QY 4571 GTCGGGAGGCTTCCTGCTGAGCTTCTTCCACAGCTTTGCTGCTGAGAGCAACACAG 4630
DB 2554 GTCGGGAGGCTTCCTGCTGAGCTTCTTCCACAGCTTTGCTGCTGAGAGCAACACAG 2613
QY 4631 CAGACGCAAGCGCGGAAAAAGGCGCATCTAACGCCTATCTAGGCTTTGGTAACTCGGAC 4690

CC	TSP-2 activity.	Query Match	61.8%;	Score 3573.6;	DB 21;	Length 3596;
XX		Best Local Similarity	99.6%;	Pred. No. 0;		
SQ	Sequence 3596 BP; 814 A; 1051 C; 1068 G; 663 T; 0 other;	Matches 3582;	Conservative 0;	Mismatches 14;	Indels 0;	Gaps 0;
QY	215	CAGGAGCTCAGCTGCAGGAGGACGAGTGGTCTGGAGGCTGGTCTCTGCTGGCTGCTGTGGGT	274			
DB	1	CAGGAGCTCAGCTGCAGGAGGACGAGTGGTCTGGAGGCTGGTCTCTGCTGGCTGCTGTGGGT	60			
QY	275	GTGGCCCCAGCAGCAAGCTGGTCAACGAGCAAAAGACACAGCACTTCGACCTTTTCAGTAT	334			
DB	61	GTGGCCCCAGCAGCAAGCTGGTCAACGAGCAAAAGACACAGCACTTCGACCTTTTCAGTAT	120			
QY	335	CAGCAACATCAACGCAAGACCATTTGGGGCCAAAGCAGTTCCGGGGGCCCGACCCCGGGCT	394			
DB	121	CAGCAACATCAACGCAAGACCATTTGGGGCCAAAGCAGTTCCGGGGGCCCGACCCCGGGCT	180			
QY	395	GCCGGCTTACCGCTTCGTGGCGCTTTGACTACATCCACCCTGACGTTGAACGAGATGACCTCAG	454			
DB	181	GCCGGCTTACCGCTTCGTGGCGCTTTGACTACATCCACCCTGACGTTGAACGAGATGACCTCAG	240			
QY	455	CAAGATCACCAAGATCATCGCGCAAGAGGGGCTTCTTCCTCAAGCGCCAGCTCAAGCA	514			
DB	241	CAAGATCACCAAGATCATCGCGCAAGAGGGGCTTCTTCCTCAAGCGCCAGCTCAAGCA	300			
QY	515	GGAGCGCAAGTCCAGGGGCAGCGTTGGTCTTGAGAGGGCCCGGTCTCTCCAGAGGCA	574			
DB	301	GGAGCGCAAGTCCAGGGGCAGCGTTGGTCTTGAGAGGGCCCGGTCTCTCCAGAGGCA	360			
QY	575	GTTCCAGATCGTCTCCAACGGCCCCGGGACACGCTGGATCTCACTACTCGATTGATTGACGG	634			
DB	361	GTTCCAGATCGTCTCCAAGTGGCCCCGGGACACGCTGGATCTCACTACTCGATTGATTGACGG	420			
QY	635	CACCCGCGATGTGCTTCCCTGGAGAGCTCGCCCTGGCTGACCTGCAGTGGAAAGACGT	694			
DB	421	CACCCGCGATGTGCTTCCCTGGAGAGCTCGCCCTGGCTGACCTGCAGTGGAAAGACGT	480			
QY	695	CACCGTCAGGTGCTGGCGAGACCTACAGCTTGCAGCTGGGCTGCGACCTCATAGGACC	754			
DB	481	CACCGTCAGGTGCTGGCGAGACCTACAGCTTGCAGCTGGGCTGCGACCTCATAGACAG	540			
QY	755	AGTTGCTCTGGACGAGCCCTTCTACGAGCACTGCAGCGGAAAAAGACCGGATGTAGCT	814			
DB	541	CTTCGCTCTGGACGAGCCCTTCTACGAGCACTGCAGCGGAAAAAGACCGGATGTAGCT	600			
QY	815	GGCCAAAGGCTCTGCCAGAGAGTCACTTACAGGGTTTGTCTCAGACGCTCCACCTAGT	874			
DB	601	GGCCAAAGGCTCTGCCAGAGAGTCACTTACAGGGTTTGTCTCAGACGCTCCACCTAGT	660			
QY	875	GTTTGAACCTCTGTGAAGATATTCTAAGCAAGAGGTTGCCAGCAGGCCAGGGAGC	934			
DB	661	GTTTGAACCTCTGTGAAGATATTCTAAGCAAGAGGTTGCCAGCAGGCCAGGGAGC	720			
QY	935	TGAGATCAAGCCCATCAGTGTAGAACACAGAGACCTCGCCCTGGCTGGCATGTGCACCAC	994			
DB	721	TGAGATCAAGCCCATCAGTGTAGAACACAGAGACCTCGCCCTGGCTGGCATGTGCACCAC	780			
QY	995	CGAGTACGTGGGCCCCAGCTCGGAGAGAGGCCCGAGGTGTGCGAACGCTCGTGCAGGA	1054			
DB	781	CGAGTACGTGGGCCCCAGCTCGGAGAGAGGCCCGAGGTGTGCGAACGCTCGTGCAGGA	840			
QY	1055	GCTGGGAAACATGCTCAGAGACTCTCGGGGCTCCAGCTCTCTGTGAACAGCTCAGGGA	1114			
DB	841	GCTGGGAAACATGCTCAGAGACTCTCGGGGCTCCAGCTCTCTGTGAACAGCTCAGGGA	900			
QY	1115	GAACCTCAAGAGAGTGTGCAATGATAACCACTTCTCTGGAGGCTCATTTGGTGCCCTCC	1174			
DB	901	GAACCTCAAGAGAGTGTGCAATGATAACCACTTCTCTGGAGGCTCATTTGGTGCCCTCC	960			
QY	1175	TAAGACAAGGAACATGTACGCTTGTGGCAGGATGGCCGGTTCCTTTGGGAAAAATGAAC	1234			

Db	961	 TAAGACAAGGAACATGTACAGCTGTCTGGCAGGATGCCGGTCTTTTTCGGGAAATGAAC	1020
Qy	1235	 GTGGGTGGTGACAGCTGCACACAGTGTACCTGCACAGAAATTTAAACACCATTTGCCACCA	1294
Db	1021	 GTGGGTGGTGACAGCTGCACACAGTGTACCTGCACAGAAATTTAAACACCATTTGCCACCA	1080
Qy	1295	 AATACACTCCCGCCCTGCACACTTCGCCCACTGCAGTCCTTTGTGGAAGGCCAATGCTGCCCC	1354
Db	1081	 AATACACTCCCGCCCTGCACACTTCGCCCACTGCAGTCCTTTGTGGAAGGCCAATGCTGCCCC	1140
Qy	1355	 TTCTCTGCCCTCCACTTCGGTGGACGGTGGAGAGGCGTGGTCTCCGTGGCGCAGAGTGGACCCA	1414
Db	1141	 TTCTCTGCCCTCCACTTCGGTGGACGGTGGAGAGGCGTGGTCTCCGTGGCGCAGAGTGGACCCA	1200
Qy	1415	 GTGCTCCGTGACGTGTGGCTCTGGGACCCAGACAGAGAGCGCGTCTGTGACGTCAACAG	1474
Db	1201	 GTGCTCCGTGACGTGTGGCTCTGGGACCCAGACAGAGAGCGCGTCTGTGACGTCAACAG	1260
Qy	1475	 CAACACCTCTCTTGGGCGCTTCGATCCAGACACGGGCTTCAGTCTCAGCAAGTGTGCACAC	1534
Db	1261	 CAACACCTCTCTTGGGCGCTTCGATCCAGACACGGGCTTCAGTCTCAGCAAGTGTGCACAC	1320
Qy	1535	 CCGCATCCGGCAGGACGGCGGCTGGAGCCACTGGTCACTTGGTCCTTCATGCTCTGTGAC	1594
Db	1321	 CCGCATCCGGCAGGACGGCGGCTGGAGCCACTGGTCACTTGGTCCTTCATGCTCTGTGAC	1380
Qy	1595	 CTGTGGAGTTGGCAATATCACAGCATTCGTCTCTGCAACTCCCGAGTCCCGCAGATGGG	1654
Db	1381	 CTGTGGAGTTGGCAATATCACAGCATTCGTCTCTGCAACTCCCGAGTCCCGCAGATGGG	1440
Qy	1655	 GGCGAAGAAATTCACAAAGGAGTGGCGGGAGACCAAGGCTGCACGGCGCCCATGCCCC	1714
Db	1441	 GGCGAAGAAATTCACAAAGGAGTGGCGGGAGACCAAGGCTGCACGGCGCCCATGCCCC	1500
Qy	1715	 AATCATGSCCGCTGAGGCCCTTGGTCCCGTGGTGGCGCTGCACGTGCACCTGTGCCCGG	1774
Db	1501	 AATCATGSCCGCTGAGGCCCTTGGTCCCGTGGTGGCGCTGCACGTGCACCTGTGCCCGG	1560
Qy	1775	 TGGGATCCGGGAGCGCACCCGGTCTGCAACAGCCCTGAGCCCTCAGTACGGAGGGGAAGGC	1834
Db	1561	 TGGGATCCGGGAGCGCACCCGGTCTGCAACAGCCCTGAGCCCTCAGTACGGAGGGGAAGGC	1620
Qy	1835	 CTGCCGTGGGGATGTGCAGGAGCGTCAGATGTGCAACAGAGAGAGCTGCCCGCTGATGG	1894
Db	1621	 CTGCCGTGGGGATGTGCAGGAGCGTCAGATGTGCAACAGAGAGAGCTGCCCGCTGATGG	1680
Qy	1895	 CTGTTTATCCAAACCCCTTGCTCCCGGAGCCAGTGCAGCAGCTTCCCGATGGGTCTCTG	1954
Db	1681	 CTGTTTATCCAAACCCCTTGCTCCCGGAGCCAGTGCAGCAGCTTCCCGATGGGTCTCTG	1740
Qy	1955	 GTCATGCGGCTCTGCGCTGTGGGCTTTTGGGCAATGGCACCCACTGTGAGACCTGGA	2014
Db	1741	 GTCATGCGGCTCTGCGCTGTGGGCTTTTGGGCAATGGCACCCACTGTGAGACCTGGA	1800
Qy	2015	 CGAGTGTGCCCTGTGTCGCCGACATCTGCTTCCACCAAGAGTGCCTCGCTGTGTCAA	2074
Db	1801	 CGAGTGTGCCCTGTGTCGCCGACATCTGCTTCCACCAAGAGTGCCTCGCTGTGTCAA	1860
Qy	2075	 CACTCAGCCTTGSCCTTCCACTTGCTGCCCTGCCCGCCCGCCGATACAGAGGGAACACGCCCT	2134
Db	1861	 CACTCAGCCTTGSCCTTCCACTTGCTGCCCTGCCCGCCCGCCGATACAGAGGGAACACGCCCT	1920
Qy	2135	 CGGGTCCGCTTGGAGCAGCCAGCAGGAAAGCAAGTGTGTGAGCCCGGAAACCCATG	2194
Db	1921	 CGGGTCCGCTTGGAGCAGCCAGCAGGAAAGCAAGTGTGTGAGCCCGGAAACCCATG	1980
Qy	2195	 CAAGACAAGACACAACTGCCACAAGCACGCGAGTGCATCTACCTGGGTACATTCAG	2254
Db	1981	 CAAGACAAGACACAACTGCCACAAGCACGCGAGTGCATCTACCTGGGTACATTCAG	2040
Qy	2255	 CGACCCCATGTACAAAGTCGAGTGCACAGGCTACCGGGCGCAGGGCTCATCTGCGG	2314

Db	2041	CGACCCCATGTACAGTGGCGATGGCCAGACAGGCTACGCGGGGCGACGGGCTCATCTCTCGGG	2100
Qy	2315	GGAGACTCGAGACTGAGCGGTGGCCCAACCTCAATCTGTGCTCGCCACCAACGCCAC	2374
Db	2101	GGAGACTCGGACCTGGAGCGGTGGCCCAACCTCAATCTGTGCTCGCCACCAACGCCAC	2160
Qy	2375	CTACCACTGCATCAAGGATAACTGCCCCCATCTGCCAAATCTTGGGCNAGGAAGACTTTGA	2434
Db	2161	CTACCACTGCATCAAGGATAAATGCCCCCATCTGCCAAATCTTGGGCNAGGAAGACTTTGA	2220
Qy	2435	CAAGGACGGATTTGGCGATGCCCTGTGATCACCATGACAAATGACGGTGTGACCGATGA	2494
Db	2221	CAAGGACGGATTTGGCGATGCCCTGTGATGACCAATGACCAATGACGGTGTGACCGATGA	2280
Qy	2495	GAAGGACAACTGCCAGCTCCTCTTCAATCCCCGCCAGGCTGACTATGACAAAGATGAGGT	2554
Db	2281	GAAGGACAACTGCCAGCTCCTCTTCAATCCCCGCCAGGCTGACTATGACAAAGATGAGGT	2340
Qy	2555	TGGGGACCGCTGTGACAACTGCCCCTTACGTGCACAACCCCTGCCCATGTCGACACAGACAA	2614
Db	2341	TGGGGACCGCTGTGACAACTGCCCCTTACGTGCACAACCCCTGCCCATGTCGACACAGACAA	2400
Qy	2615	CAATGGAGAGGGTGAGCCCTGCTCCGTGCACATTCATGGGGACGATGCTTTCATGAAACG	2674
Db	2401	CAATGGAGAGGGTGAGCCCTGCTCCGTGCACATTCATGGGGACGATGCTTTCATGAAACG	2460
Qy	2675	AGACAATTTGCCCTACGCTCTACAACACTGACACAGGACACGGATGGTGACCGTGTGGG	2734
Db	2461	AGACAATTTGCCCTACGCTCTACAACACTGACACAGGAGACACGGATGGTGACCGTGTGGG	2520
Qy	2735	GGATCACTGTGACAACTGCCCCCTGGTGCACAACCCCTGACACAGCCGACGTGGACAATGA	2794
Db	2521	GGATCACTGTGACAACTGCCCCCTGGTGCACAACCCCTGACACAGCCGACGTGGACAATGA	2580
Qy	2795	CCCTGTTGGGACACGTGTGCACAACAACGAGACATAGATGACGACGCCACCAAGACAA	2854
Db	2581	CCCTGTTGGGACACGTGTGCACAACAACGAGACATAGATGACGACGCCACCAAGACAA	2640
Qy	2855	CCAGGACAACTGCCCCCTACATCTCCAACGCCAACAGGCTGACCATGACACAGACGGCCA	2914
Db	2641	CCAGGACAACTGCCCCCTACATCTCCAACGCCAACAGGCTGACCATGACACAGACGGCCA	2700
Qy	2915	GGGGAGCGCTGTGACCCCTGATGATGACAAACGATGGCGTCCCCGATGACAGGGACAATG	2974
Db	2701	GGGGAGCGCTGTGACCCCTGATGATGACAAACGATGGCGTCCCCGATGACAGGGACAATG	2760
Qy	2975	CCGGCTTGTCTTCAACCCAGACAGGAGACATTGACAGCGTGTATGGACGGGTGATATTG	3034
Db	2761	CCGGCTTGTCTTCAACCCAGACAGGAGACATTGACAGCGTGTATGGACGGGTGATATTG	2820
Qy	3035	TAAAGATGATTTTGACAATGACAACATCCAGATATTCATGATGTGTCTCTGAAAAACAA	3094
Db	2821	TAAAGATGATTTTGACAATGACAACATCCAGATATTCATGATGTGTCTCTGAAAAACAA	2880
Qy	3095	TGCCATCAGTGAGACAGACTTCAGGAACCTTCAGATGTGCCCTTGGATCCCAAGGGAC	3154
Db	2881	TGCCATCAGTGAGACAGACTTCAGGAACCTTCAGATGTGCCCTTGGATCCCAAGGGAC	2940
Qy	3155	CACCCAAATTTGATCCCAACTGGGTCATTCGCCCATCAAGGCAAGGAGCTGTTTCAGACAGC	3214
Db	2941	CACCCAAATTTGATCCCAACTGGGTCATTCGCCCATCAAGGCAAGGAGCTGTTTCAGACAGC	3000
Qy	3215	CAACTCGACCCCGGATCGCTGTAGGTTTTCACAGTTTGGGTCTGTGGACTTCAGTGG	3274
Db	3001	CAACTCGACCCCGGATCGCTGTAGGTTTTCACAGTTTGGGTCTGTGGACTTCAGTGG	3060
Qy	3275	CACATTCACGTAACACTGACCCGGACGACACTATGCTGGCTTCGCTTTGGTTACCA	3334
Db	3061	CACATTCACGTAACACTGACCCGGACGACACTATGCTGGCTTCGCTTTGGTTACCA	3120
Qy	3335	GTCAAGCAGCCGCTTCTATGTGGTGTATGTGGAAGCAGGTGACGACAGCTACTGGGAGGA	3394
Db	3121	GTCAAGCAGCCGCTTCTATGTGGTGTATGTGGAAGCAGGTGACGACAGCTACTGGGAGGA	3180

Qy	3395	CCAGCCACACGGGCGCTATGGCTACTCCGGCGTGTCCTCAAGGTGGTGAACTCCACCAC	3454
Db	3181	CCAGCCACACGGGCGCTATGGCTACTCCGGCGTGTCCTCAAGGTGGTGAACTCCACCAC	3240
Qy	3455	GGGACGGGCGAGACCTGAGGAAACCGCGTGTGGCACACAGGGGGAACACGCGGGGCGAGGT	3514
Db	3241	GGGACGGGCGAGACCTGAGGAAACCGCGTGTGGCACACAGGGGGAACACGCGGGGCGAGGT	3300
Qy	3515	CGAACCTTATGCGACGACCCACAGGAACATTCGCTGGAAGGACTACACGGCGCTATAGGTG	3574
Db	3301	CGAACCTTATGCGACGACCCACAGGAACATTCGCTGGAAGGACTACACGGCGCTATAGGTG	3360
Qy	3575	GCACCTGACTCACAGGCCCAAGACCGGCTACATCAGAGTCTTAGTGCAATGAAGGAAACA	3634
Db	3361	GCACCTGACTCACAGGCCCAAGACCGGCTACATCAGAGTCTTAGTGCAATGAAGGAAACA	3420
Qy	3635	GGTCATGGCAGACTCAGGACCTATCTATGACCAAACTACCGTGGCGGGCGGCTGGGTCT	3694
Db	3421	GGTCATGGCAGACTCAGGACCTATCTATGACCAAACTACCGTGGCGGGCGGCTGGGTCT	3480
Qy	3695	ATTGTGCTCTCTCAAGAAATGGTCTATTCTCAGACCTCAAGTACGAATGCAGAGATAT	3754
Db	3481	ATTGTGCTCTCTCAAGAAATGGTCTATTCTCAGACCTCAAGTACGAATGCAGAGATAT	3540
Qy	3755	TTAACAAGATTGCTGCATTTCCGGCAATGCCCTGTGCATGCCATGGTCCCTAGA	3810
Db	3541	TTAACAAGATTGCTGCATTTCCGGCAATGCCCTGTGCATGCCATGGTCCCTAGA	3596
RESULT 6			
AAH34535			
ID	AAH34535 standard; cDNA; 3522 bp.		
XX	AAH34535;		
AC	AAH34535;		
XX	03-SEP-2001 (first entry)		
DT	03-SEP-2001 (first entry)		
XX	Human colon cancer antigen encoding cDNA SEQ ID NO:1617.		
DE	Human; colon cancer; colon cancer antigen; diagnosis; detection;		
XX	colorectal carcinoma; chromosome 6; ss.		
KW	Homo sapiens.		
XX	Wo200122920-A2.		
PN	05-APR-2001.		
XX	28-SEP-2000; 2000WO-US26524.		
XX	29-SEP-1999; 99US-0157137.		
PR	03-NOV-1999; 99US-0163280.		
XX	(HUMA-) HUMAN GENOME SCI INC.		
FA	Ruben SM, Barash SC, Birse CE, Rosen CA;		
XX	WPI; 2001-235357/24.		
DR	P-PSDB; AAG75130.		
XX	Nucleic acids encoding 4277 human colon cancer-associated polypeptides		
PT	useful for preventing, diagnosing and/or treating colorectal cancers -		
XX	Claim 1; Page 3236-3237; 9803pp; English.		
PS	AAH32943 to AAH37195 and AAG773514 to AAG77788 represent human colon		
XX	cancer-associated nucleic acid molecules (N) and proteins (P), where		
CC	the proteins are collectively known as colon cancer antigens. The colon		
CC	cancer antigens have cytostatic activity and can be used in gene		
CC	therapy and vaccine production. N and P may be used in the prevention,		
CC	diagnosis and treatment of diseases associated with inappropriate P		
CC	expression. For example, N and P may be used to treat disorders		


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QY 3971 CTAGAGAAACCAAGTTTGGTGATATATGAGACATTTATGTGGAGTGAAAATTTGGGCATGCC 4030
DB 1954 CTAGAGAAACCAAGTTTGGTGATATATGAGACATTTATGTGGAGTGAAAATTTGGGCATGCC 2013
QY 4031 ATTACATATGCTTTTCTGTGTTCTTTAAAGAAGTACGCTTTTACATATATAAATGTAATTA 4090
DB 2014 ATTACATATGCTTTTCTGTGTTCTTTAAAGAAGTACGCTTTTACATATATAAATGTAATTA 2073
QY 4091 CTTTATGTATTTATGTATATANGAGTTTGAAGGAATACTGTGCATAAAGCCATTATGATA 4150
DB 2074 CTTTATGTATTTATGTATATANGAGTTTGAAGGAATACTGTGCATAAAGCCATTATGATA 2133
QY 4151 AATTAGCATGAAAATATTTGCTGAACACTTTTGGTGCTTAAAGTTGTACATATTTCTTTG 4210
DB 2134 AATTAGCATGAAAATATTTGCTGAACACTTTTGGTGCTTAAAGTTGTACATATTTCTTTG 2193
QY 4211 AATTAGAGTTGCTCTACATGACACACAATCCGCTTAATAATAATTATAAACAAGGTCA 4270
DB 2194 AATTAGAGTTGCTCTACATGACACACAATCCGCTTAAATAATTATAAACAAGGTCA 2253
QY 4271 ATTCAAATTTGAAGTAAATGTTTGTAGTAAGGAGAGATTAGAAGACAACAGGCATAGCAAA 4330
DB 2254 ATTCAAATTTGAAGTAAATGTTTGTAGTAAGGAGAGATTAGAAGACAACAGGCATAGCAAA 2313
QY 4331 GACATAGCTACCGATTAACTAATCGGAACATGTAACAGATTACAAAATAAACGAAC 4390
DB 2314 GACATAGCTACCGATTAACTAATCGGAACATGTAACAGATTACAAAATAAACGAAC 2373
QY 4391 CTCCTCTGCTCTACATGAAAGCCCTCATGTGCGAGTAGAGATGCGATTTCATCAAGAA 4450
DB 2374 CTCCTCTGCTCTACATGAAAGCCCTCATGTGCGAGTAGAGATGCGATTTCATCAAGAA 2433
QY 4451 CAAACATCTCTGCAAAATGGGTGTGACGCGTTTCCAGATGTGGATTGGCAAAACCTCAT 4510
DB 2434 CAAACATCTCTGCAAAATGGGTGTGACGCGTTTCCAGATGTGGATTGGCAAAACCTCAT 2493
QY 4511 TAAGTAAAGGTTAGCAGAGCAAAAGTGGGTGCTTTAGTGTGCTGTGTGGCCGTTGTGGC 4570
DB 2494 TAAGTAAAGGTTAGCAGAGCAAAAGTGGGTGCTTTAGTGTGCTGTGTGGCCGTTGTGGC 2553
QY 4571 GTCGGGAGCTCCTGCTGAGCTTCCCTCCAGCTTTGCTGCCCTGAGAGAACAGAG 4630
DB 2554 GTCGGGAGCTCCTGCTGAGCTTCCCTCCAGCTTTGCTGCCCTGAGAGAACAGAG 2613
QY 4631 CAGACGACAGGCGCGAAAGGCGCATCTAACCGCTATCTAGGCTTTGGTAACTGCGGAC 4690
DB 2614 CAGACGACAGGCGCGAAAGGCGCATCTAACCGCTATCTAGGCTTTGGTAACTGCGGAC 2673
QY 4691 AAGTTGCTTTTACCTGATTGATGATACATTTTCATTAAGGTTCCAGTTATAAATATTTG 4750
DB 2674 AAGTTGCTTTTACCTGATTGATGATACATTTTCATTAAGGTTCCAGTTATAAATATTTG 2733
QY 4751 TTAATATTTTAAAGTACATAGATGCAATCCACTTTTACCAGTAACTTATTTTAAATA 4810
DB 2734 TTAATATTTTAAAGTACATAGATGCAATCCACTTTTACCAGTAACTTATTTTAAATA 2793
QY 4811 TGCTAGTAAACACATATGTAGTATAATTTCTAGAAAACAAACATCTAATAAGTATATAATC 4870
DB 2794 TGCTAGTAAACACATATGTAGTATAATTTCTAGAAAACAAACATCTAATAAGTATATAATC 2853
QY 4871 CTGTGAAAATATGAGGCTTGATATAATATAGGTTGTCCAGATGAAGCATGCTAGAACGCTGT 4930
DB 2854 CTGTGAAAATATGAGGCTTGATATAATATAGGTTGTCCAGATGAAGCATGCTAGAACGCTGT 2913
QY 4931 AACAGATACATAGAGATAATGAGGTTTATGATGGAACCTTATATATAATATGTTGCC 4990
DB 2914 AACAGATACATAGAGATAATGAGGTTTATGATGGAACCTTATATATAATATGTTGCC 2973
QY 4991 AGCGATTTTGTAGTCAATATTTGTTACTGTATCTATCTGCTGATATGGAATTTCTTTAA 5050
DB 2974 AGCGATTTTGTAGTCAATATTTGTTACTGTATCTATCTGCTGATATGGAATTTCTTTAA 3033
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QY 5051 TTCAAACGCTGAAACGAATCAGCATTTAGCTTGTCCAGGACACACCAATAATCAGTCAT 5110
DB 3034 TTCAAACGCTGAAACGAATCAGCATTTAGCTTGTCCAGGACACACCAATAATCAGTCAT 3093
QY 5111 GTCTAATATGCAACAAGTTTCTTTTGTGTTTGTGTTTGTGTTGTTGTTGTTT 5166
DB 3094 GTCTAATATGCAACAAGTTTCTTTTGTGTTTGTGTTTGTGTTGTTGTTT 3153
QY 5167 GCTTTAAGTTGCAATGATCTTTCTGAGGAAATAGTCACTCATCCACTCCACATAAGGG 5226
DB 3154 GCTTTAAGTTGCAATGATCTTTCTGAGGAAATAGTCACTCATCCACTCCACATAAGGG 3213
QY 5227 TTTAGTAAGAGAAGTCTGCTGTCTGATGATGATAGGGGCAAACTTTTCCCTTTC 5286
DB 3214 TTTAGTAAGAGAAGTCTGCTGTCTGATGATGATAGGGGCAAACTTTTCCCTTTC 3273
QY 5287 TGTAAATAGTCATCACAATTTCTATGCCAAACAGAACGATCCATAACTTTAGTCTTAATG 5346
DB 3274 TGTAAATAGTCATCACAATTTCTATGCCAAACAGAACGATCCATAACTTTAGTCTTAATG 3333
QY 5347 TACACATTTGCATTTTGATAAAATTAATTTTGTGTTTCTTTCCTTTCAGGTTGATCGTTG 5403
DB 3334 TACACATTTGCATTTTGATAAAATTAATTTTGTGTTTCTTTCAGGTTGATCGTTGTT 3393
QY 5404 GTTGTGTTGCTGCATTTTACTTTTGTGCGTGTGGAGCTGTATTTCCCGAGA-CAACGAA 5462
DB 3394 GTTGTGTTGCTGCATTTTACTTTTGTGCGTGTGGAGCTGTATTTCCCGAGACCAACGAA 3453
QY 5463 GCGTTGGGATACATTAATGATGAGACTGTCAACAGC 5502
DB 3454 GCGTTGGGATACATTAATGATGAGACTGTCAACAGC 3493

RESULT 7
AAZ32016
ID AAZ32016 standard; DNA; 4108 BP.
XX
AC AAZ32016;
XX
DT 10-JAN-2000 (first entry)
XX
Human METH1 related EST L07803.
DE
XX
Human; METH1; MET12; anti-angiogenic; metalloprotease thrombospondin;
KW cancer; diagnosis; hyperproliferative disorder; autoimmune disease;
KW angiogenesis inhibitor; abnormal wound healing; inflammation;
KW rheumatoid arthritis; psoriasis; endometrial bleeding disorder;
KW diabetic retinopathy; macula degeneration; haemangioma; detection;
KW arterial-venous malformation; immune deficiency; ss.
XX
OS Homo sapiens.
XX
PN WO9937660-A1.
XX
PD 29-JUL-1999.
XX
PF 22-JAN-1999; 99WO-0501313.
XX
PR 23-JAN-1998; 98US-0072298.
PR 28-AUG-1998; 98US-0098539.
XX
(TRUE/) IRUELA-ARISPE L.
PA (HAST/) HASTINGS G A.
PA (RUBE/) RUBEN S M.
XX
PI IrueLa-Arispe L, Hastings GA, Ruben SM;
XX
DR WPI; 1999-590684/50.
XX
PT New isolated metalloprotease thrombospondin polypeptides, useful for
PT treating hyperproliferative disorders, cancers or autoimmune disorders
XX
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Disclosure; Page 288-291; 457pp; English.

AA432000 and AA432001 encode, and AA449501 and AA449502 represent, human metalloproteinase thrombospondin (METH) proteins METH1 and METH2 respectively. METH1 and METH2 have been found to be potent inhibitors of angiogenesis both *in vitro* and *in vivo*. They can be used for treating cancer and other disorders related to angiogenesis including abnormal wound healing, inflammation, rheumatoid arthritis, psoriasis, endometrial bleeding disorders, diabetic retinopathy, some forms of macula degeneration, haemangiomas, and arterial-venous malformations. They may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the proliferation/differentiation, or mobilisation (chemotaxis) of immune cells. The etiology of these immune deficiencies or disorders may be genetic, somatic, such as cancer or some autoimmune disorders, acquired (e.g. by chemotherapy toxins), or infectious. They can also be used to treat inflammatory conditions, both chronic and acute conditions. The products can also be used for detection and diagnosis. AA432002 to AA432080, and AA449503 to AA449511 represent sequences given in the exemplification of the present invention.

Sequence 4108 BP; 1033 A; 1056 C; 1110 G; 909 T; 0 other;

Query Match 47.5%; Score 2745.2; DB 20; Length 4108;
Best Local Similarity 82.5%; Pred. No. 0;
Matches 3218; Conservative 0; Mismatches 673; Indels 9; Gaps 6;

226 CTGCAGGAGGCAGGATGGTCTGGAGGCTGGTCCTGCTGGCTCTGTGGTGTGGCCAGCA 285

205 CAGGTGGAGACAAGATGCTCTGGGCACCTGGCCCTGCTGGCTCTGGGCATAGGGCCAAGAG 264

286 CGCAAGCTGGTCACCAGGACAAAGACACGACCTTCGACCTTTTCAGTATCAGCAACATCA 345

265 CTTCTGCTGGTGACCAAGTCAAGGACACTTTCATTGACCTTTTCAGCATTCAGCAACATTA 324

346 ACCGCAAGACCATTEGGCGCCAAAGCAGTTCCCGCGCGCCGACCCCGCGCTGCCCGCTTACC 105

325 ACCGGAAGACCATTCGGTGCCTCCAGCAGCGTTCCAGGCCCTGACCCCGGTGCCCCCTACC

406 GCTTTGGTGGCTTTGACGTACATCCCGCCTGCACCGTCACCTCACCTCACCAAG

[illegible][illegible]

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[illegible]

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503 TGTCCAAAGGCCCCAGGGGACACATTGGACCTCAACTACTGGGTAGTAGGCAATCAGCATA 624

646 19GTC1CC1GGAGGACGTGCGCTGGCTGGCTGAGTGGAGAACGTACCGTGCAGG 705

623 CCAACTTCC TGGAGGATGTGGGCCCTGGCTGACTCC CAGTGGAGAA TGTGACTGTGCAGG 684

706 TGGCTGGCGAGACCTACAGCTTGCACGTGGGCTGCGACCTCATAGGACCAGTTGCTCTGG 765

685 TGGCCAGTGACACCTATAGCCTGTATGTGGGCTGCCGATCTTATCGACAGTGTCACCCCTGG 744

766 ACGAGCCCTTCTACGAGCACCTGCAGCGGAAAGAGCCGATGTACGTGGCCAAAGGCT 825

745 AAGAACCATTCTATGAGCAGCTAGAAGTAGACAGGAGCAGGATGTACGTGGCCAAAGGTG 804

826 CTGCCAGAGAGTCACTTCAGGGGTTTGCTTCAGAACGTCCACCTAGTGTTCGAAACT 885

805 CATCTGAGAGTCACTTCAGGGCTTGCTGCAGAAATGTCATCTCGTGTTCAGATT 864

886 CTGTGGAAGATATTCTAAGCAAGAAGGTTGCCAGCAAGGCCAGGGAGCTGAGATCAACG 945

Db	865	CTGTGGGAAGATATCTTTAAGCAAGAAAAGCTGTCAACACAGCCAGGAGCTGAAGTCAACA	924
QY	946	CCATCAGTGAACAACACAGAGACGCTGCGCCTGGGTCCGATGTCAACACCGAGTACGTGG	1005
Db	925	CCATCAGTGAACATACAGAGACTCTCCATCTGAGCCCTCACATCACCAGATCTCGTGG	984
QY	1006	GCCCCAGCTCGGAGAGAGGCCGCGAGTGTGCGAAGCCTCTGTGCGAGGAGCTTGGGAACA	1065
Db	985	TCCAGGCTGTGGAGAAAGGCACAGAGAGTGTGTACGCACCTCTCTCGAGGAGTGTAGCAACA	1044
QY	1066	TGGTCCAGGAGCTCTCGGGGCTCCACGTCTCTCGTGAACCAGCTCAGCGAGAACCTCAAGA	1125
Db	1045	TCATGAATGAGCTCTCTGGAGCTGCAGCTCATGTGTAACCAAGCTGAGCAAGAACCCTGGA	1104
QY	1126	GAGTGTCCAATGATAAACACGTTTCTTGGGAGCTCATTTGGTGGCCCTCTTAAGACAAGGA	1185
Db	1105	GAGTGTCTAGTGATAACCAAGTTCCTTTTGGAGCTCATTTGGGGCCCTCTGAAGACAAGAA	1164
QY	1186	ACATGTCCAGCTTGTGCGCAGGATGGCCGCTTCTTTCGGGAAATGAAACGTGGGTGGTGG	1245
Db	1165	ACATGTCCAGCTGTGTGCGAGGGCGGAATCTTTTCAGAAAAATGAAACCCTGGGTGGTGG	1224
QY	1246	ACAGCTGCACCACGTGTACCTGCAAGAAATTTAAACCAATTTGCCACCAAAATCACCTGCC	1305
Db	1225	ATAGTTGTACCATGATGACCTCTCAAGAAATTTAAACACGCTCTGCCATCAGATCACTGCT	1284
QY	1306	GCCCTGCAACCTGCGCCAGTCCATCTCTTGTGGAAGCGCAATGCTGCGCCTTCTGCGCTCC	1365
Db	1285	CACCTGCAACTTGTGCCAACCCATCTTTGTGGAAGCGAGTGCCTCATCTCTGTTCCAC	1344
QY	1366	ACTCGTGGAGCGGTGAGGAGGGCTGTCTCCGTGGCGAGAGTGACCCAGTGCCTCCGTGA	1425
Db	1345	ACTCTCAGACAGTGTATGAGGCGTGGTCTCCGTGGCGAGAGTGAGCCGAGTCTTCTGTCA	1404
QY	1426	CGTGTGCTCTGGGACCCACACAGAGGCGGCTCTGTGACGTCACACAGCAACACCTGCT	1485
Db	1405	CCTGTGGCTCTGGACCCACAGAGAGCGGCTTGTGATGTCACACAGCAACACCTGCC	1464
QY	1486	TGGGGCCCTCGATCCAGACACGGCTTGACGTCTGAGCAAGTGTACACCCGCAATCCGGC	1545
Db	1465	TGGGGCCCTCCATTCAGACAAGGACATGCAGCTGGGCAAAATGTGTACGAGAATCCGTC	1524
QY	1546	AGGACGGCGGCTGGAGCCACTGTCTACCTTGGTTCCTCATGTCTGTGACCTGTGAGTTG	1605
Db	1525	AGAAATGAGGCTGAGGTACACTGTCTACCTGGTCTTCATGTCTCCGTGACTTGTGAGTTG	1584
QY	1606	GCAATATACACAGCATCCGTCTCTGCAACTCCCACTCCCACTGCCAGTGGGGGCGCAAGATT	1665
Db	1585	GCAATGTCCCGGATACGTCTCTGCAACTCCCACTGCCAGTGGGGGCGCAAGAACT	1644
QY	1666	GCAAGGAGTGGCGGGAGACAAAGCCTGCAAGGGGCGCCCATGCCCAATCGATGCC	1725
Db	1645	GCAAGGAGCGGCGGGAAACCAACCTGTACGGTGTATCCGTGCCCAATGATGCC	1704
QY	1726	GCTGGAGCCCTGTGTCCCGTGTGTGGCTGTGACCTGTCCAGTGTGGGTGGGATCCGGG	1785
Db	1705	GCTGGAGCCCTGTGTCCCGTGTGTGACGCTGCACAGTTACCTGTGCTGGAGGATCCGTG	1764
QY	1786	AGCGACCCGGTGTGCAACAGCCCTGAGCCCTCAGTACGAGGGGAAGCCCTGCGTGGGGG	1845
Db	1765	AGCGCTCACGCTGTTTGAACAGCCCTGAGCCCGAGTATGAGGGAAGGACTGTGTCGGGG	1824
QY	1846	ATGTGCAGGAGCTCAGATGTGCAACAAGAGAGCTGCCCCGTGGATGGCTGTTTATCCA	1905
Db	1825	ATGTGCAGAAACACCAATGTGCAACAAGAAAGCTGGCCCTATTGATGGGTGCTTATCCA	1884
QY	1906	ACCCTCTGTTCCCGGAGGCCAGTGCAGCAGCTTCCCGCAGTGGGTCTGTGTCATCGCGCT	1965
Db	1885	ACCCTGTTTCTCGGAGCCAGTGCACAGCTTCCCTGTATGGGTCTGTGTCGTGGCT	1944
QY	1966	TCCTGCCCTGTGGGCTTCTTGGGCAATGGCAACCCACTGTGAGAGCTGGACGAGTCTGCC	2025
Db	1945	CCTGCCAGTGGGCTTCTTGGGCAATGGTACCCTGTGAGGACCTGGATGAGTGTGCTG	2004

[illegible]

Query Match 47.5%; Score 2745.2; DB 22; Length 4108;
Best Local Similarity 82.5%; Pred. No. 0;

Qy	1306	CGCCTGCAACCTCGGCCAGTCCATCTTTGTGGAAAGGGAATGCTGCCTTCCTTCCTGCCTCC	1365
Db	1385	CACCTGCAACTTGTCGAACCCCATCTTTTGTGGAAAGGGAAGTGTGTCTCATCTCTGTTCCAC	1344
Qy	1366	ACTCGGTGACCGTGTAGGAGGGCTGCTCTCCGTGGCGCAGAGTGACACCAGTGCCTCCGTGA	1425
Db	1345	ACTCTGCAGACACTGATGAGGGCTGGTCTCCGTGGCGCAGAGTGGACCGAGTGTCTGTGCA	1404
Qy	1426	CGTGTGGCTCTGGGACCCAGCAGAGAGGCCGTCTCTGTGACCTCACCAAGAACACTGCT	1485
Db	1405	CCTGTGGCTCTGGGACCCAGCAGAGAGGCCGTCTTGTGATGTCAACAGCAACACCTGCC	1464
Qy	1486	TGGGGCCCCTCGATCCAGACACAGGGCTTGAGTCTCAGCAAGTGTGACACCCGCATCCGGC	1545
Db	1465	TGGGGCCCCTCCAATTCAAGACAAGAGACATGCAGCTGGGCAAAATGTGATACGAGAATCCGTC	1524
Qy	1546	AGGAGGGCGCTGGAGCCACTGGTCACTTGCTTCACTGCTTCACTGCTGTGACACCTGTGAGTTG	1605
Db	1525	AGAAATGGAGGCTGGAGTCACTGGTCACTGGTCTTCACTGCTCGTGACTTGTGGAGTTG	1584
Qy	1606	GCAATATCACACGATCCGTCTCTGCACTCCCCAGTCCCCAGATGGGGGGCAAGAAATT	1665
Db	1585	GCAATGTCAACCGCATACGTCTGCAACTCAACAGTGCCCCAGATGGTGCAGAAACT	1644
Qy	1666	GCAAAGGAGTGGCCGGGAGACAAAGCCCTGCCAGGGCGCCCCATGCCCAATCGATGCC	1725
Db	1645	GCAAGGCGAGCGCGGGAAAACCAACCCCTGTCAAGCTGTCCGTGCCCAATTGATGCC	1704
Qy	1726	GCTGGAGCCCTCGTCCCGTGGTGGCCCTGCACCTGCACCTGTCCACTGTCCCGTGGGATCCGG	1785
Db	1705	GCTGGAGCCCTCGTCCCTTGGTCAGCCTGCACAGTTACCTGTCTGGAGGGATCCGTG	1764
Qy	1786	AGCGCACCCGGGTCTGCAACAGCCCTGAGCCTCACTACGAGGAGGAAGCCCTGCCTGGGGG	1845
Db	1765	AGCGCTCACGTGTTGCAACAGCCCTGAGCCCCAGTATGGAGGGAAGACTGTCTCGGGG	1824
Qy	1846	ATGTGACGAGAGCTCAGATGTGGAACAAGAGAGTGCCTCCCGTGGATGGCTGTTTTATCCA	1905
Db	1825	ATGTGACAGAAACACCAAAATGTGCAACAAGAAAGTGCCTTATTGATGGGTGCTTATCCA	1884
Qy	1906	ACCCCTGCTTCCGGGAGCCAGTCAGCAGACTTCCCGATGGGTCFCTGGTGCATGCCGCT	1965
Db	1885	ACCGGTGTTTTCTTGAGGCAAGTGCACAGCTTCCCTGATGGGTGCTGTGCTGTGGCT	1944
Qy	1966	TCTGCCCTGTGGCTTCTTGGGCAATGGCACCCACTGTGAGGACTGGACGAGTGTGCC	2025
Db	1945	CCTGCCAGTGGCTTCTTGGGCAATGGTACCCACTGTGAGGACCTGGATGAGTGTGCTG	2004
Qy	2026	TGGTCCCCGACATCTGCTTCTCCACAGAGGTGCCCTCGTGTGTCAACACTCAGCCTG	2085
Db	2005	TGGTCACAGATAATTGCTTCTCAACTTAACAAAGCTCCCGCTGTGTCAACACCAACCCGG	2064
Qy	2086	GCTTCCACTGCTTGCCTGCCCGCCCGATACAGAGGGAACCGCCGTCCGGGTCCGCC	2145
Db	2065	GCTTCCACTGCTTGTGTCAACACGCTACAGGGGGAACCAACCTTCCGGTGTGGCC	2124
Qy	2146	TGGAAGCAGCAAGACAGGAAAGCAAGTGTGTAGCCGGAACCCATGCAAGGACAGA	2205
Db	2125	TGGAGGATGCTAGCAGAAAAAACAAGTGTGTAGCCCAAGAGNATCCATGTAAAGGACAAGA	2184
Qy	2206	CACAAACTGCCACAAGCAGCGGAGTGCATCTACTGGGTCACTTCAGCACGCCCATGT	2265
Db	2185	CTCACAGCTGCCAAGAATGCAGAGTGCATCTACTGGCCACTTTAGTCAGCCCCATGT	2244
Qy	2266	ACAAGTCGAGTGCCAGACAGGCTACCGGGGGCAGCGGTCTATCTGGGGGAGGACTCGG	2325
Db	2245	ACAAGTGTGAGTCCCAATTTGGCTACGCAAGTGTATGGGCTCATCTGCGGGGAGGACTCAG	2304
Qy	2326	ACCTGGAGGCTGGCCCAACCTCAATCTGTGGTCTGCGCCACCAACGCAACCTTACCACGTCA	2385
Db	2305	ACCTGGATGCTGGCCCCAACACACCTGGTGTGTGCTACTAATGCCACCTTACCACGTCA	2364

[illegible]

Db 4154 TTAAA 4158

RESULT 10
AA732015

AAZ32015
ID AAZ32015 standard; DNA; 2837 BP.

XX AC AAZ32015:

XX
DT 10-JAN-2000 (first entry)

XX
DE Human METH1 related EST M64866.

XX Human; METH1; anti-angiogenic; metalloprotease thrombospondin;
 KW cancer; diagnosis; hyperproliferative disorder; autoimmune disease;
 KW angiogenesis inhibitor; abnormal wound healing; inflammation;
 KW rheumatoid arthritis; psoriasis; endometrial bleeding disorder;
 KW diabetic retinopathy; macula degeneration; haemangioma; detection;
 KW arterial-venous malformation; immune deficiency; ss.

XX
OS Homo sapiens.

XX
PN WO9937660-A1.

XX
PD 29-JUL-1999.

XX
PF 22-JAN-1999;

XX
PR 23-JAN-1998; 98US-0072298

PR 28-AUG-1998; 98US-0098539
XX

PA (TRUE/) IRUELA-ARISPE L.
PA (HAST/) HASTINGS G A.

PA (RUBE/) RUBEN S M.
XX

PI Iruela-Arispe L, Hastings GA, Ruben SM;
XX

DR WPI; 1999-590684/50.
XX

PT New isolated metalloprotease thrombospondin polypeptides, useful for
PT treating hyperproliferative disorders, cancers or autoimmune disorders
PT

PS Disclosure; Page 286-288; 457pp; English.

AAZ32000 and AAZ32001 encode, and AAY49501 and AAY49502 represent, human metalloprotease thrombospondin (METH) proteins METH1 and METH2 respectively. METH1 and METH2 have been found to be potent inhibitors of angiogenesis both *in vitro* and *in vivo*. They can be used for treating cancer and other disorders related to angiogenesis including abnormal wound healing, inflammation, rheumatoid arthritis, psoriasis, endometrial bleeding disorders, diabetic retinopathy, some forms of macula degeneration, haemangiomas, and arterial-venous malformations. They may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the proliferation, differentiation, or mobilisation (chemotaxis) of immune cells. The etiology of these immune deficiencies or disorders may be genetic, somatic, such as cancer or some autoimmune disorders, acquired (e.g. by chemotherapy or toxins), or infectious. They can also be used to treat inflammatory conditions, both chronic and acute conditions. The products can also be used for detection and diagnosis. AAZ32002 to AAZ32080, and AAY49503 to AAY49511 represent sequences given in the exemplification of the present invention.

Sequence 2837 BP; 700 A; 746 C; 788 G; 603 T; 0 other;

Query Match 32.4%; Score 1872; DB 20; Length 2837;

Best Local Similarity 82.0%; Pred. No. 0;

Matches 2157; Conservative 0; Mismatches 475; Indels 0; Gaps 0;

Qy 226 CTGCAGGAGGCAGGATGGTCTGGAGGCTGGTCTCTGTGGGCTCTGTGGGTGTGGCCAGCA 285

Db 205 CAGGTGGAGACAAGATGCTCTGGGCACTGGCCCTGGCTGGCTCTGGGCATAGGGCCAAAGAG 264
QY 286 CGCAAGCTGGTACACAGGACAAAACACAGGACCTTTGACACCTTTTCAGTATCAAGCAACATCA 345
Db 265 CTTCTGTGGTGGACCAAGCTCAAGACACATTCATTTGACCTTTTCAGATCAAGCAACATTA 324
QY 346 ACCCAAGAACCATTTGGGCGCCAAAGCAGTTCCGCGGGCCGACCCCGGGGTGCGCGCTTACC 405
Db 325 ACCGGAAGACCATCGGTGCCAAGCAGTTCCGAGGGCCCTGACCCCGGGGTGCGCCCTTACC 384
QY 406 GCTTTCGTGGCTTTGACTACATATCCACCGGTGAACGAGATGACCTCAGCAAGATCAACCA 465
Db 385 GTTTTGTACGGTTTGAATACATCCCGCCAGTTCCTTACAGAGCCCACTGAAGCAGGACGCCAAGT 504
QY 466 AGATCATGCGGCACAAGAGGGCTTCTTCTCAGCGGCCACCTCAAGCAGGACGCGCAAGT 525
Db 445 AGCTTGAAGAGAAAGAGGGCTTCTTCTTACAGAGCCCACTGAAGCAGGACGCCAAGT 504
QY 526 CCAGGGGCACGCTGTTGGCTCTGAGGGCCCGGCTCTCTCCAGAGCAGGTTTCAGATCG 585
Db 505 CTCGGGAACGCTCCTGGTGTGGAAGCCCGCGCACCTCCAGAGGCGATTTGAGATTG 564
QY 586 TCTCCAAAGCGCCCGGACACGCTGGATCTACCTACTGGAITTGACGGCACCGCGCATG 645
Db 565 TGTCCAATGGCCAGGGACACTTTGGACCTCAACTACTGGGTAGAGGCAATCAGCAT 624
QY 646 TGGTCTCCCTGGAGAGCTGGCCCTGGCTGACTGCGAGTGAAGAAAGCTACCGTGAAG 705
Db 625 CCAACTCTCTGGAGGATGTGGGCTGGCTGACTCCAGTGGGAAGAACTGACTGTGCAAG 684
QY 706 TGGCTGGGAGACCTACAGCTTGACAGTGGGCTGGGCTGGACCTCATAGGACCAAGTCTCTGG 765
Db 685 TGGCCAGTGACACCTATAGCCTGTATGTGGGCTGGATCTTATCGACAGTGTCAACCTGG 744
QY 766 ACGAGCCCTTCTACGAGCACCTCGAGCGGAAAGACCGGATGTAGCTGGCCAAAGGCT 825
Db 745 AAGAACCATTCATAGCAGCTAGAAGTAGACAGGACGAGATGTACGTGGCCAAAGGTG 804
QY 826 CTGCCAGAGAGTCACTTACGGGGTTTGTTCAGAGCTGCCACCTAGTGTGTAAGAACT 885
Db 805 CATCTCAGAGAGTCACTTCAAGGAGGCTTGTGCAAGATGTCCATCTCGTGTTCAGATT 864
QY 886 CTGTGGAAGATATTCTAAGCAAGAGGTTGCCAGCAAGCGCAGGAGCTGAGATCAAGC 945
Db 865 CTGTGGAAGATATTCTAAGCAAGAGGTTGTCAACACAGCCAGGAGCTGAAGTCAACA 924
QY 946 CCATCAGTGAACAATACAGAGACTCTCCATCTGAGCCCTCAGTCACTCACACAGATCTCGTGG 1005
Db 925 GCTTGGAGAGTCACTTCAAGCAAGAGGTTGCCAGCAAGCGTCCGCTGGTCCGATGTCCACCACCGAGTACGTGG 984
QY 1006 GCTTGGAGAGTCACTTCAAGCAAGAGGTTGCCAGCAAGCGTCCGCTGGTCCGATGTCCACCACCGAGTACGTGG 1065
Db 985 TCCAGGGTGTGGAGAGGCAAGAGGTTGTACGCATCTCCGCGAGGAGTTGAGCAACA 1044
QY 1066 TGTGTCCAGGAGCTCTCGGGGCTCACGCTCTCTGTAACCAAGCTCAGCGAGAACCTCAAGA 1125
Db 1045 TGATGATGAGCTCTGTGGACTGCACGTCATGTTGTAACCAAGCTCAGCAAGAACCTTGAGA 1104
QY 1126 GAGTGTGGAATGATAACCAAGTTCTCTGGAGCTCATTTGTTGGCCCTCTCTAAGCAAGGA 1185
Db 1105 GAGTGTCTAGTGATAACCAAGTTCTCTGGAGCTCATTTGTTGGGCTCATTTGGGGGCTCTGAGAGCAAGAA 1164
QY 1186 ACATGTGAGCTTGTGGAGAGTGGCGGTTCTTGTGGGAAATGAAACAGTGGGTGGTGG 1245
Db 1165 ACATGTGAGCTTGTGGAGAGTGGCGGTTCTTGTGGGAAATGAAACAGTGGGTGGTGG 1224
QY 1246 ACAGCTGCACACCTGTACCTGCAAGAAATTTAAACCATTTGCCACCAATCACCTGCC 1305
Db 1225 ATAGTTGTACACATGACCTTGCAGAAATTTAAACAGTGTGCCATCAGATCACCTGCT 1284
QY 1306 CGCTGCACCACTGGCGAGTCCATCTTGTGGAGGCAAGTGTGGCTTCTTCTGCTGCTC 1365
Db 1285 CACCTGCACACTTGTGCCAACCCATCTTTGTGGAGGAGGAGTGTGCTCCATCTGTTTCA 1344

QY 1366 ACTCGTGGACGCTGAGAGGGCTGGTCTCCGTGGGCAGAGTGGACCCAGTGTCTCCGTGA 1425
Db 1345 ACTCTGACAGACAGTATGAGGGCTGGTCTCCGTGGGCAGAGTGGACCCAGTGTCTCTGTC 1404
QY 1426 CGTGTGGCTCTGGGACCCAGCAGAGAGGCGGCTCTGTGAGCTCACCAGCAACACCTGCT 1485
Db 1405 CCTGTGGCTCTGGGACCCAGCAGAGAGGCGGCTCTGTGATGTCCACAGCAACACCTGCC 1464
QY 1486 TGGGGCCCTCGATCCAGACAGGCTTGCAGTCTGAGCAAGTGTGACACCCGCAATCCGGC 1545
Db 1465 TGGGGCCCTCCATTCAGACAGGACATGACGCTGGGCAAAATGTATACGAGAAATCCGTC 1524
QY 1546 AGGACGGGCTGAGGACCACTGGTTCATCTTCATGCTCTGTGACCTGTGGAGTTG 1605
Db 1525 AGAATGAGGCTGAGTCACTGGTTCACCTGGTCTTCATGCTCCGTGACTTTGTGGAGTTG 1584
QY 1606 GCAATATCACACGATCGCTCTGCAACTCCCAAGTGGCCCAAGTGGGGGCAAGAAAT 1665
Db 1585 GCAATGTCAACCGCATAGCTCTGCAACTCACCAGTGGCCCAAGTGGGGGCAAGAAAT 1644
QY 1666 GCAAGGAGTGGCCGGGAGACCAAGGCTGCCAGGGCGCCCAATGCCCAATCGATGGCC 1725
Db 1645 GCAAGGAGGCGGCGGGGAAACCAACCTGTGACGCTGATCCGTCGCCCAATTTGATGGCC 1704
QY 1726 GCTGGAGCCCTGGTCCCGTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1785
Db 1705 GCTGGAGCCCTGGTCCCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1764
QY 1786 AGCCACCCCGGCTGCAACAGCCCTGAGCTCAGTGGAGGAGGAGGCTGCTGGGGG 1845
Db 1765 AGCCCTCACGTTGTGCAACAGCCCTGAGCCCAAGTGGAGGAGGAGGCTGCTGGGGG 1824
QY 1846 ATGTGAGGAGCTGATGTGCAACAGAGGAGCTGCCCGTGGATGGCTGCTTATATCCA 1905
Db 1825 ATGTGAGAGAACACCAATGTGCAACAGAGAGTGGCTGCTTATGATGGTGGCTTATCCA 1884
QY 1906 ACCCTGCTTCCCGGAGCCAGTGGAGAGCTTCCCGATGGGTGCTGCTGCTGCTGCTGCT 1965
Db 1885 ACCCTGCTTCCCGGAGCCAGTGGAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1944
QY 1966 TCTCCCTGCTGGGCTTCTTGGGCAATGGCACCCAGTGGAGGAGCTGGACGAGTGGCC 2025
Db 1945 CTGCCAGTGGGCTTCTTGGGCAATGGTACCCAGTGGAGGAGCTGGATGAGTGGTGG 2004
QY 2026 TGTGCTCCGAGATCTGCTTCTCCACAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2085
Db 2005 TGTGTCAGAGATATTGCTTCTCAACTAACAAAGCTCCCGCTGTGTCACACCAACCCGG 2064
QY 2086 GCTTCCAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2145
Db 2065 GCTTCCAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2124
QY 2146 TGAAGCAGCAACAGCAAGCAAGTGTGTGAGCCCGGAAACCCATGCAAGGACACAGA 2205
Db 2125 TGGAGGATGTAGGACAGAAACAGTGTGTGAGCCAGAGAAATCCATGTAAAGACAGA 2184
QY 2206 CACACAACTGCAACAGCAGCGGAGTGCATCTACCTGGGTCACTTTCAGCGACCCCACTGT 2265
Db 2185 CTCACAGTGCACAGAAATGACAGTGCATCTACCTGGGCACTTTAGTACGCCCACTGT 2244
QY 2266 ACAAGTGGAGTGCACAGAGCTTACGGGGGCGAGGCTCATCTGCGGGGAGGAGTGG 2325
Db 2245 ACAAGTGTAGTGGCAGATTGGCTTACGCAAGTGTGGGCTCATCTGCGGGGAGGAGTGG 2304
QY 2326 ACCTGGAGGCTGGCCCAACCTCAATCTGGTCTGGCCCAACGCAACCTTACCCTGCA 2385
Db 2305 ACCTGGAGTGGTGGCCCAACCAACCAACCTGGTGTGTGTACTTAATGCCACCTTACCCTGCA 2364
QY 2386 TCAAGGATAACTGCCCCCATCTGCCAAATTTCTGGGAGAGAACTTTGACAAAGCAGGGA 2445
Db 2365 TCAAGGACACTGCCCCCAACTGCCAAATTTCCGGGAGGAGGATTTTGTATTAAGGATGGAA 2424

Db	745	AAGAACCAATCTCTATGAGCAGCTAGAAAGTAGACAGAGCAGAGATGTACTGCGCCAAAGGTG	804
QY	826	CTCCAGAGAGAGTCACTTTCAGGGGTTTGCTTTTCAGAAAGTCCACCTACTGTGTTGAAAACT	885
Db	805	CATCTCGAGAGTCACTTTCAGGGGCTTGCTGCAGAAATGCCATCTCGTGTTCGAGATT	864
QY	886	CTGTGAAGATATTCTTAACCAAGAAGGTTGCCAGCAAGGCCAGGGAGCTGAGATCAACG	945
Db	865	CTGTGAAGATATTCTTAACCAAGAAGCTGTCAACACAGCCAGGGAGCTGAAGTCAACA	924
QY	946	CCATCAGTGAAGAACACAGAGACGCTGCGCTGGGTCCGATGTCTACCAACCCAGTACGTGG	1005
Db	925	CCATCAGTGAACATACAGAGACTCTCCATCTGAGCCCTCATCATCACACAGATCTCGTGG	984
QY	1006	GCCCCAGCTCGGAGAGAGGCCCGAGGTGTGCGAAACGCTCGTCGAGAGCTGCGGAAACA	1065
Db	985	TCCAGGCTGTGGAGAAGGCACAGGAGTGTGTACGCACTCCTTCGCGAGGAGTTGAGCAACA	1044
QY	1066	TGCTCCAGAGCTCTCGGGGCTCCAGTTCCTCGTGAACCCAGCTCAGCGAGAACTCAAGA	1125
Db	1045	TGATGAATGAGCTCTCTGACTGCACGCTCATGGTGAACCACTGAGCAAGAACAACCTGGAGA	1104
QY	1126	GAGTGTGGAATGATAACCAAGTTTCTCTGGGAGCTCATTTGGTGGCCCTCCTTAAGACAAGGA	1185
Db	1105	GAGTGTCTAGTGAATAACAGTTTCTTTTGGAGCTCATTTGGGGGCCCTCTGAAGACAAGAA	1164
QY	1186	ACATGTCAAGTCTGCTGGCAGGATGGCCGGTCTTCTTCGGGAAAATGAACGTGGGTGGTG	1245
Db	1165	ACATGTCAAGTCTGTCAGGAGGCGGAAATCTTTTCAGAAATGCAAACTGGGTGGTG	1224
QY	1246	ACAGCTGCACCAGCTGTACTCTGAAGAAATTTAAACCAATTTGGCCACCATAACACTGCC	1305
Db	1225	ATAGTTGTACCATCACTCACTGCAAGAAATTTAAACCAAGTCTGCCATCAGATCACTGCT	1284
QY	1306	CGCTTCAACCTCGCGCAGTCCATCTTTTGTGGAAGCGAATGCTGCCCTTCTCGCCCTCC	1365
Db	1285	CACCTGCAACTTGTGCCAACCCATCTTTTGTGGAAGCGAGTGTCTCCATCTCTGTTTCCAC	1344
QY	1366	ACTCGGTGACCGGTGAGGAGGCTGCTCTCCCTGGCGCAGAGTGGACCCAGTGCCTCGTGA	1425
Db	1345	ACTCTGCAGACAGTATGATGAGGCTGCTCTCCCTGGCGCAGAGTGGACCGAGTTCCTGTC	1404
QY	1426	CGTGTGGCTCTGGGACCCAGCAGAGAGCCGGTCTCTGTGAGCTCACCAAGCAACACTGCT	1485
Db	1405	CCGTGTGGCTCTGGGACCCAGCAGAGAGCCGGTCTGTGTGATCTACCAAGCAACACTGCT	1464
QY	1486	TGGGGCCCTCGATTCCAGACACAGGCTTGCGAGTCTCAGCAAGTGTACACCCGCAATCCGGC	1545
Db	1465	TGGGCCCCCTCCATTACAGCAAGACATGACGCTGGGCAATGTATACGAAGATCCGCT	1524
QY	1546	AGGACGGCGCTGGAGCCACTGGTCACCTTGGCTTTCATGCTCTGTGACCTGTGGAGTTG	1605
Db	1525	AGAATGGAGGCTGGAGTCACTGGTCACCTGGTCTTCATGCTCCGTGACTTGTGGAGTTG	1584
QY	1606	GCAATATCACAGCATCGTCTCTCGAACTCCCAAGTGCCTCCAGATGGGGGGCAAGAATT	1665
Db	1585	GCAATGTCAACCCCATACGCTCTCTGCACTCACCACTGCCCCAGATGGGTGGCAAGAACT	1644
QY	1666	GCAAGGGAGTGGCGGGAGACAAAGCTGCCAGGCGCCCCCATGCCAATCATGCCC	1725
Db	1645	GCAAGGGCAGCGCGGGAAACCAACCTGTACGGGTGATCCGTTGCCAATCATGCCC	1704
QY	1726	GCTGGAGCCCTTGGTCCCGTGGTGGCTGCACCTGTGACCTGTGCCGGTGGGATCCGGG	1785
Db	1705	GCTGGAGCCCTTGGTCCCGTGGTGGCTGCACCTGTGACCTGTGCCGGTGGGATCCGGT	1764
QY	1786	AGCGCACCGGGTCTGCCAACGCCCTGAGCCTCACTGACGAGGGAAGGCCCTGCGTGGGGG	1845
Db	1765	AGCGCTCAGGTGTTTGCACACAGCCCTGAGCCCCAGTATGAGAGGAAGGACTGTGTCGGGG	1824
QY	1846	ATGTGAGGAGCGTCAAGTGTGCAACAGAGAGAGCTGCCCGTGGATGGCTGTTTATCCA	1905
Db	1825	ATGTGACAGAACCAAAATGTGCAACAGAGAGAGTGCCTTATGATGGGTGCTTATCCA	1884

RESULT 12

RESUL 12
AAZ32052

ID AAZ32052 standard; DNA; 5289 BP.

AA
AC
AAZ32052;XX
XX

DT 10-JAN-2000 (first entry)

XX Human METH2 related EST AB005287.
 DE
 XX
 KW Human; METH1; METH2; anti-angiogenic; metalloprotease thrombospondin;
 KW cancer; diagnosis; hyperproliferative disorder; autoimmune disease;
 KW angiogenesis inhibitor; abnormal wound healing; inflammation;
 KW rheumatoid arthritis; psoriasis; endometrial bleeding disorder;
 KW diabetic retinopathy; macula degeneration; haemangioma; detection;
 KW arterial-venous malformation; immune deficiency; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO937660-Al.
 PN
 XX
 PD 29-JUL-1999.
 XX
 XX 22-JAN-1999; 99WO-US01313.
 PF
 XX
 XX 23-JAN-1998; 98US-0072298.
 PR
 XX 28-AUG-1998; 98US-0098539.
 PR
 XX
 XX (IRUE/) IRUELA-ARISPE L.
 PA (HAST/) HASTINGS G A.
 PA (RUBE/) RUBEN S M.
 XX
 XX IrueLA-Arispe L, Hastings GA, Ruben SM;
 PI
 XX
 XX WPI; 1999-590684/50.
 DR
 XX
 XX New isolated metalloprotease thrombospondin polypeptides, useful for
 PT treating hyperproliferative disorders, cancers or autoimmune disorders
 PT
 XX
 PS Disclosure; Page 414-418; 457pp; English.
 PS
 XX
 CC AA232000 and AA232001 encode, and AAY49501 and AAY49502 represent, human
 CC metalloprotease thrombospondin (METH) proteins METH1 and METH2
 CC respectively. METH1 and METH2 have been found to be potent inhibitors of
 CC angiogenesis both in vitro and in vivo. They can be used for treating
 CC cancer and other disorders related to angiogenesis including abnormal
 CC wound healing, inflammation, rheumatoid arthritis, psoriasis,
 CC endometrial bleeding disorders, diabetic retinopathy, some forms of
 CC macula degeneration, haemangiomas, and arterial-venous malformations.
 CC They may be useful in treating deficiencies or disorders of the immune
 CC system, by activating or inhibiting the proliferation, differentiation,
 CC or mobilisation (chemotaxis) of immune cells. The etiology of these
 CC immune deficiencies or disorders may be genetic, somatic, such as
 CC cancer or some autoimmune disorders, acquired (e.g. by chemotherapy or
 CC toxins), or infectious. They can also be used to treat inflammatory
 CC conditions, both chronic and acute conditions. The products can also be
 CC used for detection and diagnosis. AA232002 to AA232080, and AAY49503 to
 CC AAY49511 represent sequences given in the exemplification of the present
 CC invention.
 XX
 XX Sequence 5289 BP; 1380 A; 1378 C; 1366 G; 1165 T; 0 other;
 SQ
 Query Match 27.7%; Score 1604.2; DB 20; Length 5289;
 Best Local Similarity 66.1%; Pred. NO. 0;
 Matches 2392; Conservative 0; Mismatches 1193; Indels 32; Gaps 4;
 QY 152 CTGCGCCCTTTCGACTCGTCGGGAACACTGNAACAGTCATCATCTCTTTTGGCA 211
 DB 72 CTGCGCCCTTTCGCGCGCGCGCGCGCTGTCATCGCGTCGCGCAAGGCTCTCTGCTGG 131
 QY 212 AACAGGAGCTCAGCTGAGGAGGAGGAGTGTCTGGAGGCTGGTCTGCTGGCTCTGTG 271
 DB 132 CACAAATAGTCCACCATGGGCTGGCTGGGACTCGGTGCTCTGCTCTGCTGCTGATGC 191
 QY 272 GGTGTGGCCAGCAGCAAGTGTTCACAGGACAAAGACAGCACTTCGACCTTTTCAG 331
 DB 192 CTGCGGCTCCACACCGCATTCACAGAGTCTGGGGGAGACACAGTGTGTTGACATCTTGA 251
 QY 332 TATCAGCAACATCAACCGCAAGACCATTTGGCGCCAGCAGTTCGCGGGCGCGCCCGG 391

DB 252 ACTACCGGAGTGTCGCGCCCAAGCGGTCTGGGCGCCGACTGGTGAAGGGCCCTGACCTTC 311
 QY 392 CQTGCGCGCTTACCGCTTCGCTGGCTTTGACTACATCTCCACCGGTGAACGAGATGACCT 451
 DB 312 TAGCCAGCTTTCGCGATCGAGATGCCAACTGATCCCGCTGTGCTGTGCTGTGCTGTG 371
 QY 452 CAGCAAGATACCAAGATCATCGCGAGAGAGGAGGCTTTCTTCTCAGCGCCAGCTCAA 511
 DB 372 CCAAGACCTAGTGGATGTGTGCGGCGGAGAAAGTTTCTCTCTCTGCTCTGCTGCTGAG 431
 QY 512 GCAGNCGCAAGTTCAGGGGACGCTGTGGCTCTGAGGGCCCGGCTCTCTCCAGAG 571
 DB 432 GCAAAATGAAGAGACCGGGGTACCTGTCTGCTGTGGAGCGGAAGACACTCTGGCCA 491
 QY 572 GCAGTTCGAGATCGTCTCAACGCGCCGCGACAGCTGCGATCTCACTACTGGATTGA 631
 DB 492 GGTCTTCAGCTGTATCTCCAAATGGCAAGCGGGCACCTTGGACCTGAGCCTGACCGTGA 551
 QY 632 CGGCACCGGCTGTGTCTCCCTGGAGAGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTG 691
 DB 552 GGGGAAGCAGCATGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 611
 QY 692 CGTACCGTGCAGGTGCTGGCGAGACCTACAGCTTTCAGCTGGGCTGGGAGCTCATAGG 751
 DB 612 CATCACCTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 671
 QY 752 ACCAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 811
 DB 672 GAATCGGAGCTGGATGTCCCATCCA -GNCATCTTCCAGGGAGCTGCTGCTGCTGCTG 730
 QY 812 COTGCGCAAGAGCTCTGCGAGAGAGTCACTC-----TTCAGGGGTTTCTGCTCAAGC 864
 DB 731 CCAGGCTCGCATTTCCAAAGGAGGTCTCAAGACAATTTCCAGGGGTTGCTGCTGCTGCT 790
 QY 865 TCCACTAGTGTTCGAAACTCTGTGGAGATATTTCTAGCAAGAGGTTGCCAGCAG 924
 DB 791 TAAGTGTGTCTTTGGAACACACCAAGAGATCTCTCAGGAACAAGAGCTGCTGCTGCTG 844
 QY 925 GCAGGGAGCTGAGATCAAGCGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 984
 DB 845 CCAGCTCTACCATGCTCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 904
 QY 985 ATGTACACCGAGTACGTGGGCGCCAGCTCGGAGAGAGGCGGAGGTGTGCTGCTGCTGCT 1044
 DB 905 CCATCGCAGCAGTACATTTGCCCAACAAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 964
 QY 1045 CTTGCGAGAGCTGGGAACATGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1104
 DB 965 CATGTGAGAGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1024
 QY 1105 AGCTCAGCGAGAACCTCAAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1164
 DB 1025 CGCTCAGGAGAGTATCCGCAAGAGTCCGAGAGAGAGAGAGAGTGGCCAGCAGTGA 1084
 QY 1165 GTGGCCCTCTTAAGACAAGAGACATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1224
 DB 1085 GGAGGCCCT-----CACCTGCTACCAACAAGAGAGTGGAGTACAGTACAGTA 1126
 QY 1225 AAATGAACAGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1284
 DB 1127 CTGGCAGAGTGGAGCGGTGGAGAGTGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1186
 QY 1285 TTTGCGACAAATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1344
 DB 1187 TCTGCAAAAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1246
 QY 1345 AATGCTGCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1404
 DB 1247 AATGCTGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1306
 QY 1405 AGTGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1464

Db 1307 AGTGGACCTCTTGTCTGTGACCTGTGGCAATGGAATCCAGCAGCGTGGCGCTCCTCGG 1366
Qy 1465 ACGTCAACCAACACCTGCTTGGGGCCCTCGATCCAGACACAGGGCTTGAGTCTGAGCA 1524
Db 1367 ACAGCCTCAACAAACAGATGTGAGGGCTCCTCTGTGCAAGCGGAGCTGCCACATCCAGG 1426
Qy 1525 AGTGTGACACCCGATCCGGCAGACAGCGGCTGAGCCACTGGTCACTTGGTCTTTCAT 1584
Db 1427 AGTGTGACAGAGATTTAAACAGAGATGGGGCTGGAGCCACTGGTCCCATGGTCACTCT 1486
Qy 1585 GCTCTGTGACCTGTGGAGTTGGCAATATCACACGATCCGCTCTCTGCAACTCCCCAGTGC 1644
Db 1487 GCTCCGTAACATGTGGAGAGCGTGTGATCACAAAGATCCGGCTCTGCAACTCCCCAGCC 1546
Qy 1645 CCCAGATGGGGGCAAGAAATGCAAAAGGAGTGGCCGGGAGACAAAGCCTGCCAGGGG 1704
Db 1547 CCCAGATGAATGGGAAGCCATGTGAGGGCAAAAGCCGGGAGACAAAGCCTGCCAGAAAG 1606
Qy 1705 CCCATGCCCAATCGATGGCGCTGGAGCCCTGGTCCCGTGGTGGCCCTGCACTGTCA 1764
Db 1607 ACTCCTGCCCATCAATGGAGGCTGGGAGCCTTGGTCACCATGGGACATCTGTTCTGTCA 1686
Qy 1765 CCTGTGCGGTGGGATCCGGGAGCGCACCCGGGTCTGCAACAGCCCTGAGCCTCAGTACG 1824
Db 1667 CCTGTGGAGGAGGGGTACAGAAACGTAGCCGGCTCTGCAACAAACCCCAACCCCAAGTTG 1726
Qy 1825 GAGGGAAGGCTGCGTGGGGATGTGAGGAGCGTCAAGTGTGCAACAAAGAGAGCTGCC 1884
Db 1727 GAGCAAGGAGTGGCTTGGTGTGATGTGACAGAAACACAGATCTGCAACAAAGCAGGAGTGC 1786
Qy 1885 CCGTGGATGGCTGTTTACCAACCCCTGCTTCCGGGAGCCAGTGCAGCAGCTTCCCG 1944
Db 1787 CCATGGAGGATGCTGTCCNATCCCTTGTGTTGTTCCAGTGTACCGCTTACCCTG 1846
Qy 1945 ATGGGTCTGTGTCAGCGCTTCTGCCCTGTGGCTTCTTGGGCAATGGCCACCACTGTG 2004
Db 1847 ATGCAGCTTGGAACTGTGGTGCCTGTCCCGCAGGCTATAGTGGAGATGGAGTCCAGTGA 1906
Qy 2005 AGGACCTGGAGAGTGTGCCCTGTGCCCGNACATCTGCTTCTCCACAGCAAGTGTGCTG 2064
Db 1907 AAGACGTTGATGTGCAAGAGATCCCTGATGCTCTTCAACCAATGGAGAGACACA 1966
Qy 2065 GCTGTGCAACACTCAGCCTGGCTTCCACTGCCTGCCCTGCCCGCCGATACAGAGGA 2124
Db 1967 GGTGTGAGACACAGACCCGGCTACAACTGCTGCTGCCCTGCCACCGGCTTCACTGGCT 2026
Qy 2125 ACCAGCCGTGGGGTGGGCTTGAAGCAGCCAAAGACGGAAAGCAAGTGTGTGAGCCGG 2184
Db 2027 CGCAGCCCTTTGGCGGGGCTGGAACATGCCACCGCCCAACAGCAGTATGCAAGCCCG 2086
Qy 2185 AAAACCATGCAAGGACAGACACAACTGCCACAGCAGCGGGAGTGCATCTACCTGG 2244
Db 2087 GAAACCCCTGCACAGAGGGGACACAGCTGCAACAAAGAGCCCAAGTGTCAACTACCTGG 2146
Qy 2245 GTCACTTCAGGACCCCATGTACAAAGTCCGAGTCCAGAGGCTACGCGGCGCAGCGGC 2304
Db 2147 GCCACTACAGCGACCCCATGTACCGCTGCGAGTGCAGGCTGGCTACGCGGCAACGGCA 2206
Qy 2305 TCATCTGCGGGAGGACTCGGACCTTGGACGGCTGGCCCAACCTCAATCTGTGTCTGCGCCA 2364
Db 2207 TCATCTGCGGGAGGACACAGACCTGGAGGCTGGCCCAATGAGGACCTGTGTGCGGTG 2266
Qy 2365 CCAAGGCCACTTACCATGTCAAGATTAAGTAACTGCCCCCATCTGCCAAATCTGGGAGG 2424
Db 2267 CCAAGCCAATCTTACCATGTCAAGAAAGATTAATTTGCCCAACCTTCCCACTCAGGGCAGG 2326
Qy 2425 AAGACTTTGACAAGGAGGATTCGGCATGCTGCTGTGATGATGAGATGACAAATACCGGTG 2484
Db 2327 AAGACTATGACAAGGATGGAATGGCGCATGCTGCGATGATGAGATGACAAATGAAGA 2386
Qy 2485 TGACCGATGAGAAGCAACTGCGCAGCTCTCTTCAATCCCGCCAGGCTGACTATGACA 2544
Db 2387 TTCAGATGACAGGACAACTGTCCATTCATTAACACCCAGCCAGTACGACTATGACA 2446

Qy 2545 AGGATAGGTTGGGACCGCTGTGCAAACTGCCCTTACGTGCCAACACCTGCCAGATCG 2604
Db 2447 GAGATACGTTGGGAGACCGCTGTGCAAACTGCCCTTCAACACCAACCCAGCAGCGTG 2506
Qy 2605 ACACAGAACAAATGTGAGAGGGTGACGCTCTCCGTGGACATTTGATGGGGACCATGTCT 2664
Db 2507 ACACAGATAACAATGGGAGGAGACGCTGTGACGTGACATTTGATGGGGACAGTATCC 2566
Qy 2665 TCAATGAACAGAGACAAATTTGTCCTTACGTCTACAACTGACACAGAGGACACGATGGT 2724
Db 2567 TCAATGAACGGGACAACTGCCAGTATGTCTAAATGTGGACCAAGAAAGACACTGACATGG 2626
Qy 2725 ACGCTGTGGGGATCACTGTGACAACTGCCCTTGGTGGTGCACAAACCTTGACAGACCGG 2784
Db 2627 ACGGGTGTGTGATCACTGTGACAACTGCCCTTGGAAACAACATCCAGACAGCTCGACT 2686
Qy 2785 TGGCAATGACCTTGTGGGACAGTGTGACAAACAGGAGACATAGATCACCAGCGCC 2844
Db 2687 CTGACTCGGACCGCATTTGGAGACACCTGTGACAAACATCAGGATATTGATGAAGACGGCC 2746
Qy 2845 ACCAGAACAAACAGGACAACTGCCCTTACATCTCCAAACGCAACAGGCTGACCATGACA 2904
Db 2747 ACCAGAACAACTGACAACTGTCCCTACGTGCCCAACGCAACAGGCTGACCATGACA 2806
Qy 2905 GAGAGCGCAGGGCAGCGCTGTGACCTGTGATGATGACAAAGATGGCTGCCCGATGACA 2964
Db 2807 AGGATGGCAAGCGGATGCGCTGTGACCATGTGACGAAATGATGATGGCATCTCTGATGACC 2866
Qy 2965 GGGACAACTGCGGCTTGTGTTCAACCCAGACAGGAGGACTTGCAGGTGATGATGACGCGG 3024
Db 2867 GGGACAACTGCGGCTGTTGCCCAATCTGACCAAGAGGACTCTGATGGTGTGATGTCAG 2926
Qy 3025 GTGATTTTGTAAAGATGATTTTGACAAATGACAACTCCCAAGATATTGATGATGTGTGTC 3084
Db 2927 GTGATGTTGCAAGATGATTTTGACCAAGGAAAGTGGCCAGACATGATGACATCTGTC 2986
Qy 3085 CTGAAACAATGCCATCAGTGAGACAGACTTCAGAACTTCCAGATGGTCCCTTGGATC 3144
Db 2987 CCGAAATGTTGATCAGTGAGACTGATTTCCGCCGATTCAGATGATTTCTCTAGATC 3046
Qy 3145 CCAAGGGACCAACAAATTTGATCCCAACTGGCTATTTCGCCCAATCAAGCAAGGAGCTGG 3204
Db 3047 CCAAGGGACATCCAGATGACCTTACTGGGTGTACGCCATCAGGGTAAAGAACTCG 3106
Qy 3205 TTCAGACGCAACTCGGACCCCGGCATCGCTGTAGTGTGACGAGTGTGGGTCTGTGG 3264
Db 3107 TCCAGACTGTCAACTGTGACCTTGGACTTGTGTAGTGTATGACGAATTTAACCGCTGG 3166
Qy 3265 ACTTCAGTGGACATTTCTACGTAACACTGACCGGGAGCAGACTATGCTGGCTTGTCT 3324
Db 3167 ACTTCAGTGGACCTTCTTCATCAACACCGAGAGGATGACGACTATGCCGGCTTGTGT 3226
Qy 3325 TTGTTTACCACTCAAGACGCGCTTCTATGTGTGATGTGGAAGCAGGTGACGAGACCT 3384
Db 3227 TTGCTTACCACTCAGACGCGCTTCTATGTGTGATGTGGAAGCAGGTGACGACTCAGTCT 3286
Qy 3385 ACTGGGAGGACCAACCCAGCGGCTTATGGCTACTCTCGGCGTGTCCCTCAAGTGTGTA 3444
Db 3287 ACTGGACACCAACCCAGCAGGCTCAGGGGTACTCTGGACTTTCCTGGAAGTTGTAA 3346
Qy 3445 ACTCCACCGGGGACGGCGGAGCACTGAGGACCGCTGTGGCACACAGGGGAACAGCC 3504
Db 3347 ACTCCACCGGGGCTGGCGAGCAGCTGCGGAATGCCCTGTGGCACACAGGAAACACT 3406
Qy 3505 CGGGCAGGTGCGAACCTTATGGCAGCAGCCCAAGCAATTTGGTGTGGAAGACTACAGG 3564
Db 3407 CTGGCAGGTGCGCACACTGTGGCATGACCTCGCTCAGTATTTGGCTGGAAGATTTCACTG 3466
Qy 3565 CCTATAGTGGCACTGACTCAGAGGCGCAAGAGCGGCTACATCAGAGTCTTACTGTGATG 3624
Db 3467 CCTACAGATGGCATCTGAGCCACAGGCCAAAGACAGGTTTTCATCAGAGTGTATGTATG 3526

QY 3625 AAGGAAACAGGTCATGGCAGACTCAGGACCTATCTATGACCAAAACCTACGCTGGCGGCGC 3684
 DB 3527 AAGGGAAGAAATCATGGCTGACTCAGGACCCATCTATGACAAAACCTATGCTGGTGGGA 3586
 QY 3685 GCGTGGGTCTATTGCTCTCTCAAGAAATGGTCTATTCTCAGACCTCAAGTACGAAT 3744
 DB 3587 GCGTAGCCTGTTGCTCTCTCAAGAAATGGTCTCTCTCCGACCTGAATATGAAT 3646
 QY 3745 GCAGAGATATTTAAACA 3761
 DB 3647 GCAGAGACTCCTAATCA 3663

RESULT 13
 AAC90309
 ID AAC90309 standard; DNA; 5289 BP.
 XX
 AC AAC90309;
 XX
 DT 19-MAR-2001 (first entry)
 XX
 DE AB005287 cDNA clone.
 XX
 KW METH; metalloprotease; thrombospondin; angiogenesis inhibition;
 KW cancer therapy; benign tumour; ocular angiogenic disease;
 KW rheumatoid arthritis; psoriasis; wound healing; endometriosis;
 KW vasculogenesis; granulation; hypertrophic scar; nonunion fracture;
 KW scleroderma, trachoma; vascular adhesion; myocardial angiogenesis;
 KW coronary collateral; cerebral collateral; arteriovenous malformation;
 KW ischaemic limb angiogenesis; Osler-Webber syndrome; wound granulation;
 KW plaque neovascularisation; telangiectasia; haemophilic joint; EST;
 KW angiofibroma; fibromuscular dysplasia; expressed sequence tag;
 KW Crohn's disease; atherosclerosis; birth control; ss.
 XX
 OS Unidentified.
 XX
 PN WO200071577-A1.
 PD 30-NOV-2000.
 XX
 PF 25-MAY-2000; 2000WO-US14462.
 XX
 PR 25-MAY-1999; 99US-0318208.
 PR 20-JUL-1999; 99US-0144862.
 PR 10-AUG-1999; 99US-0147823.
 PR 13-AUG-1999; 99US-0373658.
 PR 22-DEC-1999; 99US-0171503.
 PR 22-FEB-2000; 2000US-0183792.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (SMK) SMITHKLINE BEECHAM CORP.
 PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
 PA (IRUE/) IRUELA-ARISPE L.
 PA (HAST/) HASTINGS G A.
 PA (RUB/) RUBEN S M.
 PA (JON/) JONAK Z L.
 PA (TRUL/) TRULLI S H.
 PA (FORN/) FORNWALD J A.
 PA (TERR/) TERRETT J A.
 XX
 PI IrueLA-Arispe L, Hastings GA, Ruben SM, Jonak ZL, Trulli SH;
 PI Fornwald JA, Terrett JA;
 XX
 DR WPI; 2001-025136/03.
 XX
 PT METH1 and METH2 polynucleotides and encoded polypeptides, used to
 PT inhibit angiogenesis in the treatment of disorders such as cancer,
 PT rheumatoid arthritis and psoriasis -
 XX
 PS Claim 14; Pages 715-718; 768pp; English.
 XX
 CC The present invention relates to human METH1 and METH2, (ME for
 CC metalloprotease and TH for thrombospondin; see AAB50002 and AAB50003).

CC The present sequence is an expressed sequence tag (EST) for METH. METH
 CC can be used for inhibiting angiogenesis in an individual, and for
 CC treating cancer, benign tumours, an ocular angiogenic disease,
 CC rheumatoid arthritis, psoriasis, delayed wound healing, endometriosis,
 CC scleroderma, trachoma, vascular adhesions, myocardial angiogenesis,
 CC coronary collaterals, cerebral collaterals, arteriovenous malformations,
 CC ischaemic limb angiogenesis, Osler-Webber syndrome, plaque
 CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,
 CC fibromuscular dysplasia, wound granulation, Crohn's disease or
 CC atherosclerosis. METH can also be used in birth control. METH can also
 CC be used in diagnostic methods for the prognosis of cancer.
 XX
 SQ Sequence 5289 BP; 1380 A; 1378 C; 1366 G; 1165 T; 0 other;
 Query Match 27.7%; Score 1604.2; DB 22; Length 5289;
 Best Local Similarity 66.1%; Pred. No. 0;
 Matches 2392; Conservative 0; Mismatches 1193; Indels 32; Gaps 4;

QY 152 CTGCGCTTTCTGACTCGGTCCGGAACACTGAAACAGTCACTACATGCTCTTTTGGCA 211
 DB 72 CTGCGCTTTCTGCGCGCGCGCGCTGCATCCGCGTCCGCACAGGCTCCTTGTGG 131
 QY 212 AACCAAGGAGCTCAGCTGCAGGAGGAGGATGCTCTGGAGGCTGCTCTGCTGCTGTG 271
 DB 132 CACAATAGCTCCACCATGGGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 191
 QY 272 GGTGGGCGCCACGACGCAAGCTGGTGCACAGGACAAAGACAGCTTCGACCTTTTCA 331
 DB 192 CTGCGCTTCCAAACCCGATCCAGACTCTGGGGGAGACAAAGCTGTGTGACATCTTGA 251
 QY 332 TATACGAACATCAACCGCAAGACCATTTGGCGCCAAAGCAGTTTCCGCGGCGCCGCG 391
 DB 252 ACTCAGCGGAGCTGCCGCAAGCGTCTGGGCGCGGCTGCTGTAAGGCGCTGACCC 311
 QY 392 CGTGGCGGCTTACCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 451
 DB 312 TAGCCAGCTTTTCCGCTATCGAGGATGCCAACCTGATCCCGCTGCTGCTGCTGCTG 371
 QY 452 CAGCAAGATCACAAGATCATGCGGCAAGAGGAGGCTTCTTCCCTCAGCGCCACCTCA 511
 DB 372 CCAAGACCTAGTGGATGCTGTCGGGCGGAGAAAGTTTCTTCTCTCTGCTGCTGCTG 431
 QY 512 CGAGACGCGCAAGTCCAGGGCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 571
 DB 432 GCMAATGAAGAAGACCGCGGCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 491
 QY 572 GCAGTTCCAGATCGTCTCCAAAGCGGCGCGGACGCTGCTGCTGCTGCTGCTGCTGCT 631
 DB 492 GGTCTTACGCTGATCTCCAAATGGCAAGGCGGCGCACCTGGACCTGAGCCTGACCG 551
 QY 632 CGGCACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 691
 DB 552 GGGGAGCAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 611
 QY 692 CGTCACCGTGCAGGTGGCTGGCGAGACCTACAGCTGTGACGCTGGGCTGCTGCTGCTG 751
 DB 612 CATCACCTGTTGTGTCAGGAGGACGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 671
 QY 752 ACCAGTTCTCTGGACGAGCGCTTCTACGAGCAGCTGCTGAGGCGGAGAAAGACCGG 811
 DB 672 GAATGCGGAGTGGATGTCCTCCCATCCCA-GAGCATCTTCCACCGGAGACCTGGCC 730
 QY 812 CGTGGCCAAAGGCTCTGCGCAGAGAGTGCAC-----TTCAGGGGTTGCTTCAAGACG 864
 DB 731 CCAGGCTCCGATGCTCCCAAGAGAGGTGTCAACGACAAATTTCCAGGGGTTGCTGCA 790
 QY 865 TCCACCTAGTGTGAAACCTCTGTGGAGATATTTCTAAGCAAGAAGGTTTGGCAGCAAG 924
 DB 791 TAAGGTTTGTCTTTGGAAACACACACAGAAAGACATCTCTCAGGAACAAGGCTGC-----T 844
 QY 925 GCCAGGAGCTGAGATCAACCCCATCAGTGAGAACACAGACGCTGCGGCTGGTCCGC 984

Db 845 CCAGCTCTACCAAGTCTTTTGTACCCCTTGACAAACAGTGGTGAATGGGTCCAGCCCTG 904
QY 985 ATGTCACCAACGAGTACGTGGGCCCCAGCTCGGAGAGAGCCCGAGGTGTGCAAGCCT 1044
Db 905 CCATCCGCACACGACTACATTTGGCCACAAAGAACGACCTGCAAGCCATCTGTGGCATCT 964
QY 1045 CGTGGAGAGCTGGGAAACAGTCCAGAGCTCTCGGGCTCCAGCTGCTCTGTGAACC 1104
Db 965 CATGTGACGAGCTGTCCAGCATGGTCTGGAGCTCAGGGTCTACGCCACCATCTGTGACCA 1024
QY 1105 AGCTACGAGAGAACCTCAAGAGAGTCTGAATGATATACCAAGTTCTCTGGAGCTCATTTG 1164
Db 1025 CGTGCAGGACAGTATCCGAAGTGACCGAAGAGAACAAAGAGCTGGCCCAACGAGCTGA 1084
QY 1165 GTGGCCCTCTTAAGAACAGGAATGTACGTTGTGGCAGGATGGCCGTTCTTTTGGCG 1224
Db 1085 GGAGGCC-----CACTCTGCTACCAACAGGAGTGCAGTACAGGA 1126
QY 1225 AAAATGAACGTGGTGTGGAGAGCTGCACAGCTGCACAGCTGTACTCTCAAGAAATTTAAACCA 1284
Db 1127 CTGGCAGGAGTGGAGCGTGGAGAGCTGCACGTAGTGTGCTGCCAAGACTCAGTTTACCA 1186
QY 1285 TTTGCCACCAAAATCACCTGCCCGCTGCAACCTGCGCCAGTCCATCTTTTGTGGAGGCG 1344
Db 1187 TCTGCAAAAAGTCTCTGTGCCATCATGCCCTGCTCCATGTCACAGTTCCGGATGGAG 1246
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Db 1247 AATGCTGCCACGGTGTGCCAGGACTCTGCAGACGATGGTGTGCTGCCCTGCCGTGCTG 1306
QY 1405 AGTGGACCAAGTCTCGTCACTGTGGCTCTGGGACCCAGAGAGGCGGCTCTGTG 1464
Db 1307 AGTGGACCTCTGCTGTGACCTGTGGCAATGGAATCCAGACGCTGGCGCTCCTGCG 1366
QY 1465 ACCTCACAGCAACACCTCTGGGGCCCTCGATCCAGACAGCGGCTTGCGAGTCTGAGCA 1524
Db 1367 ACAGCTCAACACAGATGGAGGGTCTCTGTGCAGACGGGACTGCCACATCCAGG 1426
QY 1525 AGTGTGACACCGGATCCGCGAGAGCGGCTGGAGCCACTGCTACCTTGGTCTTTTAT 1584
Db 1427 AGTGTGACAAAGATTTAAACAGATGGCGCTGGAGCCACTGCTGCCCTCCATGCTCATCT 1486
QY 1585 GCTCTGTGACCTGTGGAGTTGGCAATATCACAGCATCCGCTCTGCAACTCCCACTGTC 1644
Db 1487 GCTCCGTAAACATGTGGAGAGCGGTGTGATCAAGAGATCCGGCTCTGCAACTCCCACTG 1546
QY 1645 CCCAGATGGGGGCAAGAAATGCAAGGGAGTGGCGGGAGACCAAGCCTGCCAGGCG 1704
Db 1547 CCCAGATGAATGGAGCCATGTGAGGGCAAGGCCGGGAGACCAAGCCTGCCAGAAAG 1606
QY 1705 CCCATGCCCAATCGATGGCGCTGGAGCCCTGGTCCCGCTGGTGGCGCTGCACTGTCA 1764
Db 1607 ACTCTGCCCAATCAATGGAGGTGGGACCTTGGTCACCATGGGACATGTTCTGTCTCA 1666
QY 1765 CTTGTGCGGTGGATCCGGGAGCGCACCGGTCTGCAACAGCCCTGAGCCCTGAGTACG 1824
Db 1667 CTTGTGGAGAGGGGTACAAAGAGTACGCGGCTCTGCAACAAACCCCAACCCCACTTTG 1726
QY 1825 GAGGGAAGGCTGCTGGTGGGAGTGTGCAGGAGCTGAGATGTGCAACAGAGGAGTGC 1884
Db 1727 GAGCAAGGACTGCTGTGGTGTGTGACAAACAGATCTGCAACAGAGAGTGTCT 1786
QY 1885 CCGTGGATGCTGTTTATCAACCCCTGCTCCCGGGAGCCAGTGCAGAGCTTCCCGG 1944
Db 1787 CCATTGACGATGCTGTCAATCCCTGCTTGTGGTGTCCAGTGTACAGCTACCCCTG 1846
QY 1945 ATGGCTCTGCTATGGCGCTCTGCGCTGTGGCTTCTTGGGAATGAGCCACCTGCTG 2004
Db 1847 ATGGACCTGGAAGTGTGGTGTGCTGTCCCGAGGCTATAGTGGAGATGGAGTGCAGTGA 1906
QY 2005 AGGACCTGGAGAGTGTGCCCTGTGTCGCCGACATCTGCTTCTCCACAGCAAGTGTGCTC 2064
Db 1907 AAGACGTTGATGATGCAAGAAAGATCCCTGTGCTGCTTCAACCAACAAATGGAGAGCA 1966

QY 2065 GCTGTGTCAACACTCAGCCTGGCTTCACCTGCTGCTGCTCCCGCCCGCCGATACAGAGGA 2124
Db 1967 GGTGTGAGAAACACAGACCCCGGCTTACAACTGCTGCTGCTCCACCCGCTTCACTGCT 2026
QY 2125 ACCAGCCGCTGGGTGCTGGAAGCAGCCAGAGAGGAAAGCAAGTGTGTGAGCCG 2184
Db 2027 CGCAGCCCTTTGGCGGGGCTGGAACATGCCACCCCAACAGAGGTATGCAAGCCCC 2086
QY 2185 AAAACCCATCAAGGACAAAGACACAACTGCCACAAGCAGCGGAGTGCATCTACCTGG 2244
Db 2087 GAAACCCCTGCACAGAGCGGACACAGACTGCAACAAGAGCCAAAGTGTGCAACTACCTGG 2146
QY 2245 GTCACCTTACGACGCCCATGTACAAGTGCAGTGCAGAGAGGCTACGCGGGGAGCGGCG 2304
Db 2147 GCACCTACAGCAGCCCATGTACGCTGCGAGTGCAGAGCTGCTAGCGCGCAACGCA 2206
QY 2305 TCACTCTCGGGGAGGACTCGGAGCTGGACGCTGGCCCAACCTCAATCTGCTGTCGCCCA 2364
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QY 2365 CCAACGCCACTTACCACTGCATCAAGGATAACTGCCCCCATCTGCCAAATCTTGGGCGAG 2424
Db 2267 CCAACGCCACTTACCACTGCAGAAAGGATAATTTGCCCAACCTTCCCAACTCAGGCGAG 2326
QY 2425 AAGACTTTGACAGGAGCGGATTTGGCGATGCTGTGTATGATGACAGTGAACAATGACGGTG 2484
Db 2327 AAGACTATGACAAAGGATGGAATCGCGATGCTGCGATGATGACGATGACAAATGATAAGA 2386
QY 2485 TGACCGATGAGAGGACAACTGCCAGCTCTCTTCAATCCCGCCAGGCTGACTATGACA 2544
Db 2387 TTCAGATGACAGGACAACTGTCCATTTCAACACCCAGCCAGTACGACTATGACA 2446
QY 2545 AGGATGAGTTGGGACCGCTGTGACAACTGCCCTTACGTGCAACACCCCTGCCAGATCG 2604
Db 2447 GAGTACGCTGGGAGACCGCTGTGACAACTGCCCTTACAAACCCAGCCAGACCGAGCTG 2506
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Db 2567 TCAATGAACGGGACAACTGCCAGTATGTACAATGTGGACCAAGAAACACTGACATGG 2626
QY 2725 ACGGTGGGGGATCACTGTGACAACTGCCCTGCTGGTGGACACACCCCTGACAGACCCAGC 2784
Db 2627 ACGGGTTGTGATCAGTGTGACAACTGCCCTTGGAAACAAATCCAGACCAAGCTCAGCT 2686
QY 2785 TGGACAATGACCTTTGTTGGGGACCAAGTGTGACAAACAGAGACATAGATGACAGACGCC 2844
Db 2687 CTGACTCGGACCGCATTTGGAGACACCTGTGACAAACATCAGGATATTGATGAAGACGCC 2746
QY 2845 ACCAGAACACAGGACAACTGCCCTTACATCTCCCAAGCCCAACCGGCTGACCATGACA 2904
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QY 2905 GAGACGCCAGGCGAGCCTGTGACCTGATGATGACAAAGTGGCGTCCCGATGACA 2964
Db 2807 AGATGCAAGGGGATGCTGTGACCATGATGACAAATGATGGCATTTCTGTGATGCC 2866
QY 2965 GGGACAACTCCCGCTTTGTTTCAACCCAGAGGAGACTTTGGACGGTGTGAGCGGG 3024
Db 2867 GGGACAACTCGAGCTGTGCCCAATCTTCCAGAGAGGACTCTGATGGTGTGATGGTCCAG 2926
QY 3025 GTGATATTTTAAAGATGATTTTGACAAATGACAAATCCAGATATTTGATGATGTGTGTC 3084
Db 2927 GTGATGTTTCAAGATGATTTTACCAGGACAGGTTGCCAGACATTTGATGATGATGTC 2986
QY 3085 CTGAAAACAAATGCCATCAGTGAGACAGCTTCCAGAACTTCCAGATGCTCCCTTGGATC 3144
Db 2987 CCGAAAATGTTGATATCAGTGAGACTGATTTCCCGGATTTCCAGATGATTTCTTCTAGATC 3046

	Qy	252	CTGGTCCTGCTGGCTCTGTGGGTGTGGCCCAACGACAGCATGGTACCACGAGACAAGAC	311
	Dd	139	CTTTCTTGATGCATGTGTGTGGACCAACCGCATTCACAGACTGTGGCGGAGACA---AC	195
	Qy	312	ACGACCTTCGACCTTTTCAGTATCAGCAAAATCATCAACCGCAAGACCATTTGCCGCCAAGCAG	371
	Dd	196	AGCGTGTTCGACATCTTTGAATCATCCGGGGCCCGCCCAAGGGGTGTGGCGCGCACGTG	255
	Qy	372	TTCGGGGGGCCCGACCCCGGGGTGGCGGCTTACCGCTTCGTGGCGTTTGACTACATCCCA	431
	Dd	256	GTGAAGGGCCCCGACCTTCAGGCCAGCTTTCGCGATCGAGGATGCCAACCTGTATCCC	315
	Qy	432	CCGGTGAACGCAAGATGACCTCAGCAAGAATCACCAAGATCATCGCGCAAGAGAGGCTTC	491
	Dd	316	CCTGTCCCTGTATGACAACTTCCAAGACCTGTGTGGATGCTGTGGGGGAGAAAAGGCTTC	375
	Qy	492	TTCCTCACGGCCCACTCAAGCAGGACGGCAAGTCAAGGGCGACGCTGTGTGGCTCTGGAG	551
	Dd	376	CTCCTTCTGGCATCTCTGAGGCAGATGAAGAAGACCGCGGGCACGCTGTGGCCCTGGAG	435
	Qy	552	GGCCCCGGTCTCTCCACAGAGCAGTTCCGAGATCGTCTTCAAACGCCGCCCGCGGACACGCTG	611
	Dd	436	CGGAAGACCACTCTGCGCCAGSTCTTCAGCGTGTGTCCATGCGCAAGGCGGCGACCCCTG	495
	Qy	612	GATCTCACTACTGATTGACGGCAACCGGCATGTGGTCTCCCTGGAGGACGTTCGGCCCTG	671
	Dd	496	GACCTCAGGCTGACCGTCCAAAGAAAGCAGCACGTCGTGTCTGTGGAAGAAGCTCTCCCTG	555
	Qy	672	GCTGACTCGAGTGAAGACGTCACCGTGCAGGTGGCTGGCGAGACCTACAGCTTGCAC	731
	Dd	556	GC AACGGCGCAGTGAAGAGCATCACCTGTTGTGCGAAGACAGGGGCCACGCTGTAC	615
	Qy	732	GTGGGTCGGACCTCATAGGACCAAGTTGCTCTGACGAGCGCTTCTACGAGCACCTGCGAG	791
	Dd	616	ATCGACTGTAAAAATCGGAATGTCTGAGTTGGACGCTCCCATCCAAAGCGTCTTCACC	675
	Qy	792	GGGGAAGAGCCGGATGTACGTGGCCMAAGGCTC-----TGCCAGAGAGATCACTTTC	845
	Dd	676	AGAGACTGGCCAGCATCGCCAGACTCCGCATCGCA AAGGGGGCTCAATGACAATTTTC	735
	Qy	846	AGGGGTTGCTTCAGAACGTCACCTAGTGTTTGAAAACHTCTGTGGAAGATATTTTAAGC	905
	Dd	736	CAGGGGGTGTGCAAAATGTGAGGTTGTCTTTGGAACCAACACAGAAGACATCTCTCAGG	795
	Qy	906	AAGAAGGTTGTCAGCAAGGCCAGGAGCTGAGATCAACGCCATCAGTGAAGAACACAGAG	965
	Dd	796	ACA AAGCTGC-----TCCAGCTTACAGTGTCTCTCTCACTTGCACACACAGTG	849
	Qy	966	ACGCTGCGCGTGGGTFCGCATGTGCACACCGAGTAGCTGGGGCCCCAGCTCGGAGAGGAG	1025
	Dd	850	GTGAATGTGTTCCAGCCCTTGCATCCGCACTAACCTTACATTTGCCCAAGACAAAGGACTTG	909

PI Nojima H, Ioshisue H, Obayashi M, Uta T, Kugata A, Kawabata A, Sakurada K, Kuga T, Sekine S, Nakamura Y, Sugano S;

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Qy 1026 CCCGAGGTGTGCGAACGCTCGTGGAGGAGCTGGGAACATGGTCCAGGAGCTCTCGGGG 1085
Dy 910 CAAGCCATCTCGCGCATCTCTGTGATGAGCTGTCCAGCATGGTCTCGAACTCAGGGGC 969
Qy 1086 CTCACAGTCTCTGCTGAACACCTCAGCGAGAACCTCAAGAGAGTGTGCAATGATAACCG 1145
Dy 970 CTGCGCACCATGTGTACCAAGCTCCAGGACAGATCCGCAAGTGTACTGAAGAGAACAA 1029
Qy 1146 TTTCTCTGGGAGCTCATGTGTGGCCCTCTTAAGACAAAGAACATGTTCAGCTTGTGCGAG 1205
Dy 1030 GAGTTGGCCAAATGAGCTGAGCGGCCCTC-----CCCTATGCTATCAC 1071
Qy 1206 GATGGCCGGTCTTTGGCGGAAATGAACAGTGGGTGGTGGACACTGCACCACTGTGTACC 1265
Dy 1072 AACGGAGTTCAGTACAGAAATTAACGAGGAATGGACTGTGTATAGCTGCACACTGAGTGTAC 1131
Qy 1266 TGCAGAAATTTAAACCATTTGCGCACCAATCACTTCCCGCTGCAACCTTCGCCAGT 1325
Dy 1132 TGTGAGAACTCAGTTACCATCTGCAAAAAGTGTCTTGCCCATCATGCCCTGCTCCAA 1191
Qy 1326 CCATCTTTTGGGAAGGAAATGTGCCCTTCTCTGCCCTCCACTCGGTGGAGCGGTGAGGAG 1385
Dy 1192 GCCACAGTCTCTGATGGAGAATGCTCTCGCTGTGGCCACGCACTCTGCGGACGAT 1251
Qy 1386 GGCTGGTCTCGGTGGGAGAGTGGACCCAGTGTCTCGGTGAGCTGTGGCTCTGGGAACCGAG 1445
Dy 1252 GGCTGGTCTCCATGGTCCGAGTGGACCTCTCTGTTCTACGAGCTGTGGCAATGGAATTCAG 1311
Qy 1446 CAGAGAGCGCGGTCTGTGAGCTCACCAGCAACACCTCTTGGGGCCCTCGATCCAGACA 1505
Dy 1312 CAGCGCGCGCTCTCGGATAGCTCAACAAACCGATGTGAGGCTCTCTCGGTCCAGACA 1371
Qy 1506 CGGCTTTGAGCTGTGAGCAAGTGTGACACCGCATCCGCGAGGACGGCGGTGGAGCCAC 1565
Dy 1372 CGGACCTGCCACATTCAGGAGTGTGACAAAAGATTTAAACAGGATGTGGCTGGAGCCAC 1431
Qy 1566 TGGTCACTTGGTCTTATGCTGTGACCTGTGGATGTGGATGTGCCATATCAGACGATCGGT 1625
Dy 1432 TGGTCCCGTGGTCTATGTTGTCTGTGACATGTGGTGTGATGGTGTGATCAACAAGATCCGG 1491
Qy 1626 CTCGTCAACTCCCAGTCCCGAGATGGGGGCAAGAATTCAAAGGAGTGGCGGGAG 1685
Dy 1492 CTCGTCAACTCCCAGCCCAAGATGAATGGGAACCTGTGAAGGCGAAGCGGGAG 1551
Qy 1686 ACCAAGCCTGCCAGGGGCCATGCCCAATCGATGCCCTGGAGCCCTGGAGCCCTGTCGCCG 1745
Dy 1552 ACCAAGCCTGCAAGAAAGACGCTGCCCATCAATGGAGCTGGGTCTGGGTTCACCA 1611
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Dy 1612 TGGGACATCTGTTCTGACCTGTGGAGGAGGGGTACAGAACTAGTCTCTCTGCAAC 1671
Qy 1806 AGCCCTGAGCTCAGTACGGGAAGGCGCTGCTGGGGATGTGCAGGAGCGTGCAGATG 1865
Dy 1672 AACCCCGCACCCAGTTTGGAGGCAAGGACTGGCTTGGTGTATGAACAGAAACAGATC 1731
Qy 1866 TGCAGCAAGAGAGCTGCCCGTGGATGGCTGTTTATCCAAACCCCTGCTTCCCGGGAGCC 1925
Dy 1732 TGCAGCAAGAGAGCTGTCCAAATGTATGATGATGCTGTCCAACTCCCTGCTTGGCGGGGTG 1791
Qy 1926 CAGTGCAGCAGCTTCCCGATGGTCTCTGTGTCATGCGGCTCTGCCCTGTGGGCTTCTTG 1985
Dy 1792 AAGTGTACTAGCTACCCCTGATGGAGCTGGAAATGTGGTGTCTGCCCTCGGTTACAGT 1851
Qy 1986 GGCAATGGCACCCACTGTGAGGACCTGGACGAGTGTGCCCTGGTCCCGGACATCTGTTTC 2045
Dy 1852 GGAATGGCATCCAGTGCACAGATGTTGATGAGTGCAGAGTGCCTGATGCCTGCTTC 1911
Qy 2046 TCCACCAAGAGGTCCTCGCTGTGTCAACACTCAGCCTGGCTTCCACTGCTGCCCTG 2105
Dy 1912 AACCACAATGGAGACACCGGTGTGAGAACACAGGACCCCGGCTACAACTGCGCTGCCCTGCG 1971

Qy 2106 CCGCCCGATACAGAGGAACACGCGGTGGGGTGGAGCAGCAACGACGAA 2165
Dy 1972 CCCCACGCTTACCGGCTACAGCGCTTCGGCCAGGGGTGTGCAACATGTCCACGCGCAAC 2031
Qy 2166 AAGCAAGTGTGTAGCCCGGAAACCCATGCAAGGACAAGACACAACTGCCACAAGCAC 2225
Dy 2032 AAACAGGTGTCAAGCCCGGTAAACCCCTGCACAGATGGGACCCAGGACTGCAACAAGAAC 2091
Qy 2226 GCGAGTGCATCTTACCTGGGTCACTTCAGCGACCCCATGTATCAAGTGGGAGTGGCAGACA 2285
Dy 2092 GCCAAGTGCMACTACCTGGGCCACTATAGCGACCCCATGTACCGCTGCGAGTGAAGCCT 2151
Qy 2286 GGCTACCGGCGGACGCGCTCATCTCGGGGAGGACTCGGACCTGGAGGCTGGCCCAAC 2345
Dy 2152 GGCTACGCTGGCAATGGCATCATCTCGGGGAGGACACAGACCTGGATGGCTGGCCCAAT 2211
Qy 2346 CTCATCTGTCTCGGCCACCAACGCCACCTTACCACATCATCAAGGATAAAGTGCACCCCAT 2405
Dy 2212 GAGAACCTGGTGTGGTGGCCAAATGCGACTTACCACCTGCAAAAAGGATAATTTGCCCAAC 2271
Qy 2406 CTGCCAAATCTGGGCAAGGAGATTTGACAAGGACGGGATTTGGCGATGCTCTGATGAT 2465
Dy 2272 CTTCCCAACTCAGGCGAGGAAGACTATGACAAGGATGGAATTTGGTGTGCTGTGATGAT 2331
Qy 2466 GACCATGACAAATGACGGTGTGACCGATGAGAGGACAACTGCCAGCTCTCTTCAATCCC 2525
Dy 2332 GACCATGACAAATGAAAAATTTCCAGATGACAGGACAACTGTCCATTCATTAACCCCA 2391
Qy 2526 CGCCAGGCTGACTATGACAAGGATGAGGTGGGACCGCTGTGACAACTGCCCTTACCTG 2585
Dy 2392 GCTCAGTATGACTATGACAGAGATGATGTGGGAGACCGCTGTGACAACTGTCCCTACAC 2451
Qy 2586 CACAACCTGCCAGATCGACAGACAAACAAATGAGAGGCTGACGCTGTCTCGGTGGAC 2645
Dy 2452 CACAACCCAGATCAGGCGAGACACAGACAACAATGGGAAGGAGACGCTGTGCTGCAGAC 2511
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Dy 2512 ATTGATGGAGCGGTATCTCTCAATGAACGGGACAACTGCCAGTACGCTTACAAATGTGGAC 2571
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Dy 2572 CAGAGACACTGATATGGATGGGTGGAGATCAGTGTGACAATTTGCCCTTGGAAAC 2631
Qy 2766 AACCTGACACAGACGAGTGGACAATGACCTTGTGGGGACCACTGAGTGTGACAACAACGAG 2825
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Dy 2872 TCTGACGCGGATGTCGAGGTGATGCTGCAAAAGATGATTTTGACCATGACAGTGTGCCA 2931
Qy 3066 GATATTGATGATGTGTCTCTGAAAACAATGCCATCAGTGAGACAGACTTCAGGAACATTC 3125
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QY 1026 CCCAGGTGTCCGAACGCTGTGCGAGGAGCTGGGAACATGTGTCAGGAGCTCTCGGG 1085
DB 910 CAGCCATCTGCGGCACTCTCTGTGTGAGCTGTCCAGCATGTGTCCTGGAACCTCAGGGGC 969
QY 1086 CTCACATCTCTGTGAACCACTCAGCGAGAACCTCAAGAGAGTGTGCAATGATAACCGAG 1145
DB 970 CTGGCACCATTGTGACCACTGCGAGCAGCATCCGCAAGTACTGAAGAGAACAA 1029
QY 1146 TTTCTCTGGGAGCTCAATGTGTGGCCCTCTTAAGACAAGAACATGTGAGCTTGTCTGCGAG 1205
DB 1030 GAGTTGGCCAAATGAGCTGAGCGGCCCTC-----CCCTATGCTATCAC 1071
QY 1206 GATGGCCGGTTCTTTGCGGAATATGAACGTGGTGTGGACAGCTGCACCACTGTATACC 1265
DB 1072 AAGCGAGTTCAGTACAGANAATACGAGGAATGGACTGTGATAGCTGCATGAGTGTCA 1131
QY 1266 TGAAGAATTTTAAACCATTTGCGCCACCAATCACTCCCGCTGCAACCTGCGCCAGT 1325
DB 1132 TGTGAGAACTCAGTTACCATCTGCAAAAAGGTGTCTTCCGCCCCATCATGCCCCCTGCTCCA 1191
QY 1326 CCATCTCTTGTGAAGCGAATGTCCTCTCTGCTTCCCTGCTGAGCGGTGAGGAG 1385
DB 1192 GCCACAGTTCCTGTGAGAGATGCTGCTCGCTGTTGGCCACGCACTCTGCGGACGAT 1251
QY 1386 GGCTGGTCTCCGTGGGAGAGTGGACCCAGTGTCTCCGTGAGCGTGTGCTTGGACCCAG 1445
DB 1252 GGTGTGCTCCATGGTCCGAGTGACCTCTCTGTCTACGAGCTGTGGCAATGGAAATTCAG 1311
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QY 1626 CTCTGCAACTCCCGAGTGCCTCAGATGGGGGCAAGAAATTCGAAAGGAGTGGCCGGGAG 1685
DB 1492 CTCTGCAACTCTCCAGCCCCAGATGAATGGGAAACCCCTGTGAAGCGGAAGCCGGGAG 1551
QY 1686 ACCAAAGCCTGCCAGGCGCCCATGCCCAATCGATGGCGCTGGAGCCCTGTGTCGCCG 1745
DB 1552 ACCAAAGCCTGCCAGAAAGACGCTGCCCATCAATGAGGCTGGGGTCTTGTGTACCA 1611
QY 1746 TGGTGGCTTCGACTGTACCTGTGCGGTGGGATCCGGGAGCGCACCCCGGTGTGCAAC 1805
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QY 1806 AGCCCTGAGCTCAGTACGAGGAAGGCTGCTGTGGGGATGTGAGGAGCGTCAGATG 1865
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DB 1792 AAGTTTACTAGTACTAGCTGATGGAGAAATGTGGTGTCTTCCCTCGGTGTACAGT 1851
QY 1986 GGCAATGGCAGCCCACTGTGAGGAGCTGGACGAGTGTGCCCTGGTCCCGAGCATCTGCTTC 2045
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QY 2046 TCCACCAGAGTGTCTGCTGTCAAACTCAGCCTTGGCTTCCACTGCTGCTGCCCTGC 2105
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QY 2106 CCGCCCCGATACAGAGGGAACCGCTCGGGGTGCGGCTGGGAAGCAGCCAAAGCGAA 2165
DB 1972 CCCCACAGCTTACCGGCTCACAGGCTTGGCCAGGGGTGCGAACATGTCACGCGCCAAAC 2031
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DB 2272 CTTCCTCAACTCAGGGCAGGAAGACTATGACAAGGATGGAATTTGGTGTGCTGTGATGAT 2331
QY 2466 GACGATGACANTGACGGTGTGACCGATGAGAAGACAACTGCCAGCTCTCTTCAATCCC 2525
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QY 2586 CACAACCTTCCCAAGTGCACACAGACAACAAATGAGAGGGTGGCGCTGCTTCCGTGGAC 2645
DB 2452 CACAACCCAGATCAGGACAGACACAGACAACAATGGGAAGGAGACGCGCTGTGCTGCAGAC 2511
QY 2646 ATTCATGGGAGCAGTGTCTTCAATGAACGACAGACAATTTGTCCCTAGCTTACAACACTGAC 2705
DB 2512 ATTCATGGAGACGATATCTCAATGACGGGACAACTGCCAGTACGCTTACAAATGTGGAC 2571
QY 2706 CAGAGGACACGGATGGTGGGGATGACGGTGTGAGGATCAGTGTGACAACCTGCCCTGTGAC 2765
DB 2572 CAGAGACACTGATATGGATGGGGTGGAGATCAGTGTGACAATTTGCCCTTGGAAACAC 2631
QY 2766 AACCTTGACACAGACCGCTGGACAAATGCTTGTGGGACCACTGTTGAGCAACAACAG 2825
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Db 2992 CAGATGATTCCTCTGGACCCCAAGGGACATCCCAAAATGACCTTAACCTGGGTGTTAGCC 3051
QY 3186 CATCAAGCAAGAGCTGTTTCAGACAGCAACTCGGACCCCGGCATCGCTAGGTTTT 3245
Db 3052 CATCAGGTAAAGAACTCGTCCAGACTGTCAACTGTGATCTCTGGACTCGCTGTAGGTTAT 3111
QY 3246 GACGAGTTTGGGCTCTGTGACTTTCAGTGGCACAATTCAGTAAACACTGACCGGACGAC 3305
Db 3112 GATGAGTTTAAAGCTGTGACTTTCAGTGGCACCCTTCTCATCAACACCAAGGACCGAT 3171
QY 3306 GACTATGCTGGCTTCGTCTTTGGTTACCAAGTCAAGACGCCGCTTCTATGTGGTGAATGG 3365
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Search completed: December 27, 2002, 00:33:28
Job time : 772 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 27, 2002, 00:19:39 ; Search time 124 Seconds
(without alignments)
14304.987 Million cell updates/sec

Title: US-09-919-770-3
Perfect score: 5784
Sequence: 1 acggatccagtcacagagg.....aattgtataaaagggttttt 5784

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents.NA.*
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2: /cgn2.6/ptodata/1/lna/5B_COMB.seq.*
3: /cgn2.6/ptodata/1/lna/6A_COMB.seq.*
4: /cgn2.6/ptodata/1/lna/6B_COMB.seq.*
5: /cgn2.6/ptodata/1/lna/PTUS_COMB.seq.*
6: /cgn2.6/ptodata/1/lna/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	559.4	9.7	3074	5	Sequence 3, Appli
2	526.4	9.1	2820	5	Sequence 1, Appli
3	255.8	4.4	1326	3	Sequence 4, Appli
4	252.8	4.4	857	3	Sequence 2, Appli
5	162.8	2.8	270	1	Sequence 43, Appl
6	162.8	2.8	270	1	Sequence 136, App
7	162.8	2.8	270	1	Sequence 143, App
8	104.2	1.8	390	4	Sequence 7, Appli
9	88.6	1.5	1926	4	Sequence 4, Appli
10	88.6	1.5	1931	2	Sequence 2, Appli
11	64.2	1.1	5163	3	Sequence 1, Appli
12	64.2	1.1	5163	3	Sequence 4, Appli
13	64.2	1.1	5318	3	Sequence 2, Appli
14	64.2	1.1	5318	3	Sequence 3, Appli
15	61.2	1.1	5511	3	Sequence 2, Appli
16	61.2	1.1	7334	3	Sequence 1, Appli
17	60.2	1.0	3489	2	Sequence 1, Appli
18	60.2	1.0	3489	4	Sequence 1, Appli
19	60.2	1.0	32207	2	Sequence 20, Appl
20	60.2	1.0	32207	4	Sequence 20, Appl
21	60.2	1.0	32207	4	Sequence 20, Appl
22	58.4	1.0	3675	4	Sequence 3, Appli
23	58.4	1.0	4042	4	Sequence 5, Appli
24	54.2	0.9	4192	4	Sequence 1, Appli
25	53.8	0.9	3624	1	Sequence 6, Appli
26	53.8	0.9	3624	2	Sequence 6, Appli
27	53.8	0.9	3624	3	Sequence 6, Appli

28	53.8	0.9	3624	3	US-08-459-504B-6	Sequence 6, Appli
29	53.8	0.9	3624	3	US-08-459-444-6	Sequence 6, Appli
30	53.8	0.9	3624	3	US-09-053-549-7	Sequence 7, Appli
31	53.8	0.9	3624	4	US-09-547-422-6	Sequence 6, Appli
32	52.4	0.9	2831	2	US-08-808-982-3	Sequence 3, Appli
33	52.4	0.9	2831	4	US-09-306-902A-3	Sequence 3, Appli
34	52.4	0.9	3014	2	US-08-808-982-1	Sequence 1, Appli
35	52.4	0.9	3014	4	US-09-306-902A-1	Sequence 1, Appli
36	52.2	0.9	150	2	US-07-829-461A-8	Sequence 8, Appli
37	52	0.9	5852	1	US-07-867-106-2	Sequence 2, Appli
38	51.6	0.9	3126	4	US-09-392-184-7	Sequence 7, Appli
39	50.2	0.9	2889	1	US-08-537-002A-4	Sequence 4, Appli
40	50.2	0.9	2889	3	US-08-863-010-4	Sequence 4, Appli
41	50.2	0.9	2889	4	US-09-024-429-4	Sequence 4, Appli
42	50.2	0.9	3600	1	US-08-537-002A-5	Sequence 5, Appli
43	50.2	0.9	3600	3	US-08-863-010-5	Sequence 5, Appli
44	50.2	0.9	3600	4	US-09-024-429-5	Sequence 5, Appli
45	50.2	0.9	4403765	4	US-09-103-840A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
PCT-US93-11725-3
; Sequence 3, Application PC/TUS9311725
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMAN THROMBOSPONDIN-4
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield, & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 inch
; COMPUTER: IBM-compatible
; OPERATING SYSTEM: MS-DOS Version 3.3
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11725
; FILING DATE: filed herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/985,296
; FILING DATE: 04-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, Edward R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: B0801/7005WO
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3074 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ANTI-SENSE: no
; PCT-US93-11725-3

Query Match	9.7%	Score 559.4;	DB 5;	Length 3074;
Best Local Similarity	62.1%	Pred. No. 2.4e-124;		
Matches	928;	Conservative	0;	Mismatches 546;
				Indels 21;
				Gaps 2;
QY	2271	TGGAGTGGCCAGACAGCTACGGGGGCGGGGCGGCTATCTCGGGGAGGACTCGGACCTG	2330	
Db	1369	TGTGTGTGTGGAGTCGGCTTGGCTGGAGATGCTATCTGTGGAAGGATGTGGACATC	1428	
QY	2331	GACGGCTGGCCCAACCTCAATCTGCTGCGCCACGACGACCTACCACCTGATCAAG	2390	
Db	1429	GACAGTTACCCCGACGAAGAACTGCCATGCTCTGCCA-----GGAAGCTGAAAAAG	1479	

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 QY 2451 GATGCTCTGATGATGACGATGACAAATGACGGTGTGACCGATGAGAGGACAACTGCCAG 2510
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 DB 1720 GCCTGATGATGATGATGGATGGAGATGGAATAAAAAACATCTTGGNCAACTGGCCAAA 1779
 QY 2691 GTCTACAACTGACAGAGGACACGAGTGTGACGGTGTGGGGATCACTGTGACAAAC 2750
 DB 1780 TTTCCCATCTGACCAACGGGACAGATGGTGTGTGGGGATGCCGTGTGACAGT 1839
 QY 2751 TGCCCCCTGGTGACAAACCTTGACAGACCGACGTGGGCAATGACCTTTGTTGGGACAG 2810
 DB 1840 TGTCTGATGTGACGACCAACCTTAACGACTGTGATGTGGATATGATCTGTTGGGGACTCC 1899
 QY 2811 TGTGACAAACAGGAGATGATGACAGCGCCACGACCAACAGGACCACTGACCTGCC 2870
 DB 1900 TGTGACCAATCAGGACGATGTGGATGGGACCGACAGGACGACAGCAACTGCCCC 1959
 QY 2871 TACATCTCCAAACGACAGGCTGACCATGACAGACAGCGCCAGCGCCCTGTGAC 2930
 DB 1960 ACCGTATTACAGTGGCCAGCTGACACCCGATGAAGATGGAATGGTGACGATGTGAT 2019
 QY 2931 CCTGATGATGACAGGATGGCGTCCCGA-----TGRAGGGACAATGCCGG 2978
 DB 2020 GATGATGATGACATGATGTATCCAGACCTTGTGCGCCCTGGACCAACAATGCCGG 2079
 QY 2979 CTGTGTTTCAACCCAGACGAGGAGCTTGGACGGTGTGACGGGTGATTTGTATAA 3038
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 DB 2500 CCAFTCCGAGAGTTGCAGAACCTGGCATTCAGCTCAAGGCTGTGAAGTCTAAGACAGGT 2559

QY 3459 ACGGCGGAGACCTCGAGGAACCGCTGTGGACACACCGGGGAAACACCGCGGGCAGGTGCA 3518
 DB 2560 CCAGGCGAGCATCTCCGGAACCTCCCTGTGGCACACGGGGGACACACAGTCAACAGGTGAG 2619
 QY 3519 ACCTTATCGCAGGACCCAGGACAACTTGGCTGGAAGGACTACACGGCTATAGTGGCAC 3578
 DB 2620 CTGCTGTGGAAGGACTCCAGGAATGTGGCTGGAAGGACAAAGGTCTCTACCGCTGGTTC 2679
 QY 3579 CTGACTCAGGCCCCAAGACCGGCTACATCAGATCTTAGTGCATGAAGGAAACAGGTTC 3638
 DB 2680 CTACAGCACAGCCCCAGGCTGGCTACATCAGGTACCATTTTATGAAGGCTCTGAGTTG 2739
 QY 3639 ATGGCAGACTCAGGACCTATCTATGACCAAACTAGCTGGCGGGCGCTGGGTCTATTT 3698
 DB 2740 GTGGCTGACTCTGGCTCACCATACACCAACAATCGCTGGAGGCGGACTTGGCGCTTTTC 2799
 QY 3699 GTCTTCTCTCAAGAAATGGTCTATTTCTCAGACCTCAAGTACGAATGACAGATA 3753
 DB 2800 TGCTTCTCTCAAGAAACATCATCTGGTCCAACTCAAGTATCGCTGCAATGACA 2854

RESULT 2
 PCT-US93-11725-1
 ; Sequence 1, Application PC/TUS9311725
 ; GENERAL INFORMATION:
 ; APPLICANT:
 ; TITLE OF INVENTION: HUMAN THROMBOSPONDIN-4
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Wolf, Greenfield, & Sacks, P.C.
 ; STREET: 600 Atlantic Avenue
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: United States of America
 ; ZIP: 02210
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3 1/2 inch
 ; COMPUTER: IBM-compatible
 ; OPERATING SYSTEM: MS-DOS Version 3.3
 ; SOFTWARE: WordPerfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US93/11725
 ; FILING DATE: filed herewith
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/985,296
 ; FILING DATE: 04-DEC-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: GATES, Edward R.
 ; REGISTRATION NUMBER: 31,616
 ; REFERENCE/DOCKET NUMBER: B0801/7005WO
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2820 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; ANTI-SENSE: no
 ; ORIGINAL SOURCE:
 ; ORGANISM: Xenopus laevis
 ; DEVELOPMENTAL STAGE: Stage 45 (germ line)

PCT-US93-11725-1
 Query Match 9.1%; Score 526.4; DB 5; Length 2820;
 Best Local Similarity 61.9%; Pred. No. 1.9e-116;
 Matches 858; Conservative 0; Mismatches 516; Indels 12; Gaps 1;
 QY 2380 ACTGCATCAAGGATAACTGCCCCCATCTGCCAAATTTCTGGCAGGAGAACTTTGACAAG 2439
 DB 1235 ACTGCAAAAAGGACAACTGTGTATATGTTCTAACTCGGGTCAAGAGACACTGATAAG 1294
 QY 2440 ACGGGATGGCGATGCCTGTGATGACGATGACGATGACGCTGTGACCCATGAGAGG 2499

Db 1295 ATAACTGGAGATGCTTGTGATGAAGATGCGGATGGAGATGGTATCCTTAATGACGAG 1354
QY 2500 ACAACTGCCAGCTCCCTTCATATCCCGCCAGCTGACTATGACAAAGATGAGGTTGGG 2559
Db 1355 ACAACTGTGTGGCTGCCAATCGATCAGAAAAACAGTGACCAAGATATATTTGGGG 1414
QY 2560 ACCGTGTGACACTGCCCTTACCTGTCACAAACCCCTGCCAGATCGACAGACAAATG 2619
Db 1415 AGCCGTGTGACACTGCCCTTACCTGTCACAAACCCCTGCCAGATCGACAGACAAATG 1474
QY 2620 GAGAGGTTGACGCTCTCCGTGGACATTCGATGGGACGATGTCTTCAATGACGAGACA 2679
Db 1475 GGAAGAGAGATGCTTGTGACGATGACATGGATGGATGGCATCAAGATATCTTGATA 1534
QY 2680 ATTGTCCTTACGCTTACAACTGACCAAGGACACGAGGATGAGCGTGTGGGGATC 2739
Db 1535 ACTGCCAGAGATTCCTCAATGTTGGACAGAAAGACAAAGATGGAGTGGTGTGATA 1594
QY 2740 ACTGTGACAACTGCCCTTGTGTCACAAACCCCTGACCAAGCAGCGTGGACATGACCTTG 2799
Db 1595 TATGTGACAGCTGTCTTGACATCATATAATCAAAACAGTCAGACATGTGACAATGACCTTG 1654
QY 2800 TTGGGACACAGCTGTGTCACAAACAGGACATAGATGACGACGCCACCAAGACCAACGAG 2859
Db 1655 TTGGAGATTCCTGTGATACCTAACAGACAGCGATGCTGTGTCACAGGACAGACAG 1714
QY 2860 ACAACTGCCCTTACATCTCCACGCCCAACAGCTGACCATGACAGACAGCGCCAGGGG 2919
Db 1715 ACAACTGCCCTTACATCTCCACGCCCAACAGCTGACCATGACAGACAGCGCCAGGGG 1774
QY 2920 AGCCCTGTGACCTGTGATGACAGAGATGGCTGCCCTTACCTTCCCTCCCGACCTG 2967
Db 1775 ATGAATGTGACGATGATGATGAATGAAGTGAATCCCGGATACCTGTCTCCCTCCCGACCTG 1834
QY 2968 ACAACTGCCCTTGTGTCACAAACAGGACATAGATGACGAGCTTGGACGGTGTGACGGGGT 3027
Db 1835 ATAACTGTAACCTGTGTCACAAACAGGACATGATGACGAGCTTGAATGAGTGGAG 1894
QY 3028 ATATTTGTAAGATGATTTGACATGACAAATCCAGATATGATGATGATGATGATGATG 3087
Db 1895 AGCTGTGTGAGCCGATTTTTCACAGGACAGCTGATGACCGAATTTGACCTTGGCTTG 1954
QY 3088 AAAACAATGCCATCAGTGAGACAGACTTCAGGAACCTTCAGAGTGGTCCCTTGGATCCCA 3147
Db 1955 AAAATGACAGATACCCCTGACAGATTTTCAGAGCTTTATCAAACTGTAGTCTGGATCCCG 2014
QY 3148 AAGGGACCAACCAATGATCCCACTGGGTCTATTCGCCATCAAGCAAGAGCTGGTTC 3207
Db 2015 AAGGAGATGCCCAATGATCCCACTGGATTTTGAACAGGAAATGGAGATGTGC 2074
QY 3208 AGACGCCAATCTGACGACCGGATCGCTGATGATGATGATGATGATGATGATGATGATG 3267
Db 2075 AGACGATGAACAGTGAACCTGACCTGGAGTGGCTTACACAGCATTTAATGAGTGTAT 2134
QY 3268 TCAGTGGACATCTACGTAACACTGACCGGACGACGACATATGCTGCTGCTGCTTGG 3327
Db 2135 TCAGGGGACATTCACGCTGAACACCATGACCGGATGATGATGATGATGATGATGATGATG 2194
QY 3328 GTTACAGTCAAGACCGCTTCTATGTTGATGATGGAAGCAGGTGACGACGACCTACT 3387
Db 2195 GTATACAGGACATTCACACTTTTATGTTGATGATGGAAGCAGACTGACGACGACTACT 2254
QY 3388 GGGAGACACGCGGACGCGGCTATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3447
Db 2255 GGCAGGCAACCCCTTCAGAGCAGTGTGACAGCTTGAATCCAACTGAAGGCTGTGAAT 2314
QY 3448 CCACACGGGGAGCGGACGACCTGAGGAACCGCTGTGGGACACGCGGGACACCGCGG 3507
Db 2315 CCAAGTCAAGGACCGGGGAACATCTGAGGAACCGCTGTGGGACACAGAGACACCAATG 2374
QY 3508 GCGAGTGGAACTTATGTCGACGACGACCCCAAGCAATTTGGCTGGAAGAGGACTACACGGCT 3567
Db 2375 ATCAAGTGAAGCTGCTCTGGAAGACCCCAAGNATGTCGGCTGGAAGCAAGTCTCCT 2434

QY 3568 ATAGTGGCACCTGACTCACAGGCCCAAGACCGCTACATCAGAGTCTTTAGTGCATGAAG 3627
Db 2435 ACCGCTGGTCTTACAGCACAGGCCCAAGTGGCTACATCAGAGCCAGATTTTATGAAG 2494
QY 3628 GAAACAGGTATGGCAGACTCAGGACCTATCTATGACCAAACTAGCTGGCGGGGGC 3687
Db 2495 GCACCGAGCTGGGTGGCTGACTGTGGAGTCACTGTGGACACACCATGCGGAGGAGAGAC 2554
QY 3688 TGGGTCTATTTGCTCTCTCAAGAAATGCTTATTTCTCAGACCTCAAGTACGAATGCA 3747
Db 2555 TGGGATTTCTCTTTTCACAGAAACATAATTTGGTCCATCTCAATACCGGTGTA 2614
QY 3748 GAGATA 2753
Db 2615 ATGATA 2620

RESULT 3

US-08-985-526-4
; Sequence 4, Application US/08985526
; Patent No. 6080728
; GENERAL INFORMATION:
; APPLICANT: Mixson, James A
; TITLE OF INVENTION: CARRIER:DNA COMPLEXES CONTAINING DNA
; TITLE OF INVENTION: ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Connolly, Bove, Lodge, & Hutz
; STREET: 1220 Market Street, P.O. Box 2207
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: U.S.A.
; ZIP: 19899
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,526
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/608,845
; FILING DATE: 16-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: McMorow Jr., Robert G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 658-9141
; TELEFAX: (302) 658-5613
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1326 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-985-526-4

Query Match 4.4%; Score 255.8; DB 3; Length 1326;
Best Local Similarity 64.7%; Pred. No. 1.1e-51;
Matches 380; Conservative 0; Mismatches 207; Indels 0; Gaps 0;

QY 1225 AAAATCAACGTTGGGTGGACAGCTGCACACGCTGTACCTCAAGAAATTTAAACCA 1284
Db 80 ATACAGGAGTAAGTGTGTGATGCTGCTGAGTGTCTACTGTGACAGACTAGTTACCA 139
QY 1285 TTTCGCCCAAAATCACTGCTCCCGCTGCACACTGCGCGCAGTCCATCCTTTGTGGAAGCG 1344
Db 140 TCTGCAAAAAGGTGCTCTGCCCATCATGCGCTGCTCCATGCGCAGTTCCTGATGGAG 199
QY 1345 AATGCTGCCCTTCTCTGCCCTCCACTCGGTGACGGTGAGGAGGCTGGTCTCCTGGGCGAG 1404

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Db 200 AATGCTGCTCGTGTGGCCAGCGACTCTGGGACGATGGCTCCATGGTCCG 259
Qy 1405 AGTGACCCAGTGTCCGTGACGTGTGGGACCCAGCAGAGAGCGCGGTCTGTG 1464
Db 260 AGTGACCTCTGTCTACGAGCTGTGCAATGGAATTCACGAGCGCGCTCTGTG 319
Qy 1465 ACGTACACGACCAACCTGTGGGGCCCTCGATCCAGACAGGGCTGTGAGTGTGAGCA 1524
Db 320 ATAGCCTCAACACCGATGTGAGGGCTCTCGGTCCAGACACGGACCTGCCACATTCAGG 379
Qy 1525 AGTGACACCCGATCCGGGACGACGCGCTGGAGCCCTGTGACCTGTGCTTCAT 1584
Db 380 AGTGACCAAAAGATTTAAACAGGATGTGCTGGAGCCACTGTGCCGCTGGTCACTT 439
Qy 1585 GCTGTGACCTGTGGAGTTGGCAATATCACACGATCCGCTCTGCAACTCCCGAGTC 1644
Db 440 GTTCTGTGACATGTGTGATGTGTATCACAAGATCCCGCTCTGCAACTCTCCAGCC 499
Qy 1645 CCCAGATGGGGGCAAGAAATTTGCAAGGGAGTGCCGGGAGACCAAGCCCTGCCAGGCG 1704
Db 500 CCCAGATGAATGGGAAACCCCTGTGAAGGCGAAGCGCGGAGACCAAGCCCTGCCAAGAA 559
Qy 1705 CCCATGCCCAATCGATGGCGCTGGAGCCCTGCTGCTCCCGTGTGCGCTGTCACTGCA 1764
Db 560 ACGCCTGCCCATCAATGGAGGCTGGGTCTCTGGTCCACATGGGACATCTGTCTGTCA 619
Qy 1765 CCTGTGCGGTGGATCCGGGAGCGACCCCGGTCTGCAACAGCCCT 1811
Db 620 CCTGTGGAGGAGGTACAGAAACGTAGTCTCTGCGTGCAGCTCT 666

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RESULT 4

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US-08-985-526-2
; Sequence 2, Application US/08985526
; Patent No. 6080728
; GENERAL INFORMATION:
; APPLICANT: Mixson, James A
; TITLE OF INVENTION: CARRIER:DNA COMPLEXES CONTAINING DNA
; TITLE OF INVENTION: ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Connolly, Bove, Lodge, & Hutz
; STREET: 1220 Market Street, P.O. Box 2207
; City: Wilmington
; STATE: Delaware
; COUNTRY: U.S.A.
; ZIP: 19899
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,526
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/608,845
; FILING DATE: 16-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: McMorow Jr., Robert G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 658-9141
; TELEFAX: (302) 658-5613
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 657 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-985-526-2

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Query Match 4.4%; Score 252.8; DB 3; Length 657;
Best Local Similarity 64.9%; Pred. No. 4.1e-51;
Matches 374; Conservative 0; Mismatches 202; Indels 0; Gaps 0;
Qy 1225 AAATGAACCTGGTGGTGCACAGCTGCACACGCTGACCTGTACCTGCAAGAAATTTAAACCA 1284
Db 80 ATAACGAGGAATGGACTGTGATAGCTGCACCTGAGTGTCTGCTGCAATGCCACATTTCTGATGAG 139
Qy 1285 TTTCGCCAAATCACCTGCGCCGCTGCAACCTGCGCCAGTCCATCTTTGTGGAAGCG 1344
Db 140 TCTGCAAAAAGTGTCTGCCCCCATCATGCTGCTGCTGCAATGCCACATTTCTGATGAG 199
Qy 1345 AATGCTGCCCTTCTGCTCCACTCGGTGGAGCTGGAGGGCTGTGCTCCGTGGGCGAG 1404
Db 200 AATGCTGCTCTGCTGTGGCCAGCGACTCTGCGGAGGATGGTGTCTCCATGGTCCG 259
Qy 1405 AGTGACCCAGTGTCCGTGACGTGTGGCTGTGGAGCCAGCAGAGCGCGGTCTGTG 1464
Db 260 AGTGACCTCTGCTGTACGAGCTGTGGCAATGGAATTCACAGCGCGCGCTCTGTG 319
Qy 1465 ACGTACACGACCAACCTGTGCGGCCCTCGATCCAGACACGGCTTGCAGTCTGAGCA 1524
Db 320 ATAGCCTCAACACCGATGTGAGGGCTCTCGTCCAGACAGGACCTGCCACATTCAGG 379
Qy 1525 AGTGACACCCGATCCGGGACGCGCTGTGAGCCACTGTGACCTTTGGTCTTCAT 1584
Db 380 AGTGACAAAGATTTAAACAGGATGTGCTGGTGGAGCCACTGTGCCCGTGGTCACTT 439
Qy 1585 GCTGTGACCTGTGGAGTGGCAATATCACACGATCCGCTCTGCAACTCCCGAGTGC 1644
Db 440 GTTCTGTGACATGTGTGATGTGATCACAAGGATCCCGCTCTGCAACTCTCCAGCC 499
Qy 1645 CCCAGATGGGGGCAAGAAATTTGCAAGGGAGTGCGCGGAGACCAAGCCCTGCCAGGCG 1704
Db 500 CCCAGATGAATGGGAAACCCCTGTGAAGGCGAAGCGCGGAGACCAAGCCCTGCCAAGAA 559
Qy 1705 CCCATGCCCAATCGATGGCGCTGGAGCCCTGCTGCTCCCGTGTGCGCTGTCACTGTCA 1764
Db 560 ACGCCTGCCCATCAATGGAGGCTGGGTCTCTGGTCCACATGGGACATCTGTCTGTCA 619
Qy 1765 CCTGTGCGGTGGATCCGGGAGCGACCCCGGTCT 1800
Db 620 CCTGTGGAGGAGGTACAGAAACGTAGTCTCTCT 655

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RESULT 5

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US-08-594-031-43
; Sequence 43, Application US/08594031
; Patent No. 5783182
; GENERAL INFORMATION:
; APPLICANT: THOMPSON, Timothy C.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
; NUMBER OF SEQUENCES: 175
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BAKER & BOTTS, L.L.P.
; STREET: 1299 Pennsylvania Avenue, N.W.
; City: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004-2400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/594,031
; FILING DATE: 30-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/006,838
; FILING DATE: 16-NOV-1995

```



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; ATTORNEY/AGENT INFORMATION:
; NAME: Remenick, James
; REGISTRATION NUMBER: 36,902
; REFERENCE/DOCKET NUMBER: 0A146-01110
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-639-7700
; TELEFAX: 202-639-7890
; TELEX:
; INFORMATION FOR SEQ ID NO: 136:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 270 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; US-08-594-031-136

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[illegible]

RESULT 7
US-08-594-031-143
; Sequence 143, Application US/08594031
; Patent No. 5783182
; GENERAL INFORMATION:
; APPLICANT: THOMPSON, Timothy C.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
; NUMBER OF SEQUENCES: 175
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BAKER & BOTTS, L.L.P.
; STREET: 1299 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004-2400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/594,031
; FILING DATE: 30-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/006,838
; FILING DATE: 16-NOV-1995

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; ATTORNEY/AGENT INFORMATION:
; NAME: Remenick, James
; REGISTRATION NUMBER: 36,902
; REFERENCE/DOCKET NUMBER: 0A146-0110
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-639-7700
; TELEFAX: 202-639-7890
; TELEX:
; INFORMATION FOR SEQ ID NO: 143:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 270 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; US-08-594-031-143

Query Match      2.8%; Score 162.8; DB 1; Length 270;
Best Local Similarity 87.6%; Pred. No. 1e-29;
Matches 212; Conservative 0; Mismatches 27; Indels 3; Gaps 3;

QY 3511 AGTTCGGAACCTTATGGCAGCAGCCAGACATTTGGCTGGAAGACTACAGGCGCTATA 3570
DB 6 AGGTCGGAGCTCTATGGCATGACCCCAAAACATTTGGCTGGAAGATTACACTGCTACA 65

QY 3571 GTTGCCACTGACTCACAGGCCCAAGACCGGCTACATCAGAGTCTTAGTGATGAAGAA 3630
DB 66 GTTGCCACTGATTCACAGGCTTAGACAGGCTACATGAGAGTCTTAGTGATGAAGAA 125

QY 3631 AACAGGTCATGGCAGACTCAGGACCTATCTATGACCAACCTACGCTGGCGGCGCTGG 3690
DB 126 AGCAAGTCATGGCTGACTCAGGACCAATTTATGACCAACCTACGCTGGCGGCGCTGG 185

QY 3691 GTCTATTGTTCTCTCTCAAGAAATGGTCTATTCTTCAGACCTCAAGTACGAATGCAG 3750
DB 186 G-CGTGTTGTTCTCTC-CAAGAGATGGTCTA-TTCTCGGACCTCAAGTATGATGCAGAG 242

QY 3751 AT 3752
DB 243 AT 244

RESULT 8
US-09-197-649-7
; Sequence 7, Application US/09197649
; Patent No. 6194550
; GENERAL INFORMATION:
; APPLICANT: Gold, Larry
; APPLICANT: Tuerk, Craig
; APPLICANT: Pribnow, David
; APPLICANT: Smith, Jonathan D.
; TITLE OF INVENTION: Systematic Polypeptide Evolution by Reverse Translation
; FILE REFERENCE: NEX02/CI-CON
; CURRENT APPLICATION NUMBER: US/09/197,649
; EARLIER FILING DATE: 1998-11-23
; EARLIER FILING DATE: 1997/829,461
; EARLIER FILING DATE: 1992-01-31
; EARLIER FILING DATE: 07/739,055
; EARLIER FILING DATE: 1991-08-01
; EARLIER FILING DATE: 07/561,968
; EARLIER FILING DATE: 1990-08-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 390
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequence

; OTHER INFORMATION: having a 120 repeat of ACG flanked by fixed
; OTHER INFORMATION: fragments having NcoI restriction sites.
US-09-197-649-7

Query Match      1.8%; Score 104.2; DB 4; Length 390;
Best Local Similarity 55.0%; Pred. No. 1.4e-15;
Matches 205; Conservative 0; Mismatches 168; Indels 0; Gaps 0;

QY 2595 GCCCAGATCGACACAGACAATGGAGAGGTGCGCTGCTGCGTGGACATTTGATGGG 2654
DB 3 GCCATGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 62

QY 2655 GACGATGCTTCAATGAACAGAGACAATTTGCTCCTAGCTTACAACTAGCAGAGGAC 2714
DB 63 GACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 122

QY 2715 ACGGATGTTGAGGGTGTGGGATCAGTGTGACAACTGCTGCTGCTGCTGCTGCTGCTGCTG 2774
DB 123 GACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 182

QY 2775 CAGACCGACGTGGACAATGACCTTTGTTGGGACCACTGTGTGACAAACAGGACACATAGAT 2834
DB 183 GACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 242

QY 2835 GACGAGCGCCACAGAACACACAGGACAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2894
DB 243 GACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 302

QY 2895 GACCATGACAGAGCGGCGCAGGGGACGCTGCTGACCCCTGATGATGACAACTGCTGCTG 2954
DB 303 GACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 362

QY 2955 CCCGATGACAGGG 2967
DB 363 GACGAGCGCATGG 375

RESULT 9
US-09-249-585A-4/c
; Sequence 4, Application US/09249585A
; Patent No. 6417002
; GENERAL INFORMATION:
; APPLICANT: Horlick, Robert
; TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISODES
; FILE REFERENCE: 0867/0D905
; CURRENT APPLICATION NUMBER: US/09/249,585A
; CURRENT FILING DATE: 1999-02-11
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 1926
; TYPE: DNA
; ORGANISM: Epstein Barr Virus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1926)
; OTHER INFORMATION: template strand of EBNA-1 DNA
US-09-249-585A-4

Query Match      1.5%; Score 88.6; DB 4; Length 1926;
Best Local Similarity 47.3%; Pred. No. 1.9e-11;
Matches 302; Conservative 0; Mismatches 334; Indels 3; Gaps 1;

QY 2418 GGGCAGGAAGACTTTGACAAGCAGCGGATTTGGCGATGCTGCTGATGATGACGATCACAAT 2477
DB 961 GAGCAGCAGGACGGGAGGAGGAGCAGCAGCAGCGGGGAGGACGAGGAGGAGGAGGAGGAG 902

QY 2478 GACGGTGTGACCGATGAGAAGACAACCTGCGAGTCTCTTCAATCCCGCCAGGCTGAC 2537
DB 901 GACGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 842

QY 2538 TATCACAAGGATGAGTTGGGACCGCTGTGACAACTGCTGCTGCTGCTGCTGCTGCTGCTG 2597
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Db	841	GACGAGCGGGAGACGGGAGAGGACGAGGACGGGAGGACGGGAGGACGAGGAC	782
Qy	2598	CAGATCGACACAGACAACAATGGAGAGGTGACGCCTGCTCCGTGGACATTTGATGGGAC	2657
Db	781	GGGAGGACGGGAGGACGAGACGCGGGAGGACGGGAGGACGAGGACGGGAGGACGAG	722
Qy	2658	GATGCTTCAATGAACAGACACAATTTGCTCCCTACGTCCTACAACACTGACACGAGGACAG	2717
Db	721	GACGGGAGGACGAGGACGGGAGGACGAGGACGGGAGGACGGGAGGACGGGAGGAGG	662
Qy	2718	GATGGTGACGCTGGGGGATCACTGTGACAACCTGCCCCCTGGTGACAACCCCTGACCAG	2777
Db	661	GACGAGGACGGGAGGACGAGGACGGGAGGACGGGAGGACGGGAGGACGGGACGGG	602
Qy	2778	ACCGAGTGGACAAATGACCTTTGTTGGGACCAAGTTGTGACACACGAGGAGCAATGATGAC	2837
Db	601	GAGGAGGACGAGGACGGGAGGACGGGAGGACGGGAGGAGGACGAGGACGGGAGGAC	542
Qy	2838	GACGGCCACCAGAAACACGAGCAACCTGCCCTCATCTCCACGCCCAACGAGCCTGAC	2897
Db	541	GGGAGGAGGACGAGGACGGGAGGAGGACGAGGACGGGAGGACGGGAGGACGGGAG	482
Qy	2898	CATGACAGAGACGGCCAGCGGACGCCTGTGACCTCATGATGATGACACAGCATGGCGTCCCC	2957
Db	481	GAGCACGAGGACCGGGAGGACCGGGAGGAGGACGAGGACGGGAGGAGGACGAGGACGGG	422
Qy	2958	GATGACGAGCAACATTCGCGCTTGTGTCAACCCACGACACGAGGAGACTTGGACGGTGAT	3017
Db	421	GAGACGGGAGGACCGGGAG---GAGGACGAGGACGGGAGGAGGACGAGGACGGGAG	365
Qy	3018	GGACGGGTGATATTTGTAAGATGATTTTGACAATGAC	3056
Db	364	GACGGGAGGACGGGAGGACCGGGAGGAGGACGAGGACGAGGAC	326

```

RESULT 10
US-09-130-114-2/c
; Sequence 2, Application US/09130114
; Patent No. 5976807
; GENERAL INFORMATION:
; APPLICANT: Horlick, Robert A.
; APPLICANT: DamaJ, Bassam B.
; APPLICANT: Robbins, Alan K.
; TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Genes
; TITLE OF INVENTION: From Multiple Transfected Episomes
; FILE REFERENCE: 0867/ID9030US1
; CURRENT APPLICATION NUMBER: US/09/130,114
; CURRENT FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: fastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: EBNA
US-09-130-114-2

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Query Match	1.5%;	Score 88.6;	DB 2;	Length 1931;
Best Local Similarity	47.3%;	Pred. No. 1.9e-11;		
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QY 2418	GGG CAGGAAGACTTTGACAGGACGGGATGGCGATGCTGTGATGATGACGATGACAAAT	2477		
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QY 2478	GACGGTGTGACCGATGAGAGGACATGCCAGTCTCTTTCAATCCCGCCAGCGCTGAC	2537		
Db 901	CACGGGAGGACGAGGACGGGGAGGACGGGAGGACGAGGACGGGGAGGACGGGGAGGAG	842		
QY 2538	TATGACAGGATGAGTTGGGACCGGTGTGACAACTGCCCTTACGTTCACAAACCTTGCC	2597		
Db 841	GACGAGGACGGGGAGGACGGGGAGGACGAGGACGGGGAGGACGGGGAGGACGAGGAC	782		
QY 2598	CAGATCAGACAGACAAATGAGAGGGTGACGCCCTGCTCCGTGGACATTTGATGGGGAC	2657		

[illegible]

	Query Match	1.1%	Score 64.2	DB 3	Length 5163
	Best Local Similarity	43.7%	Pred. No. 2.4e-05		
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Qy	2265	TACAAAGTCGAGTGCCACAGACGGCTACCGGGGACGGGCTCATCTGCGGGAGGACTCG	2324		
Db	553	TAAATGTGTTGGAGTGGAAACACACAAACAAACAACTACTACTACTACTACTACTAC	612		
Qy	2325	GACCTGGACGGCTGGCCCCAACCTCAATGTGCTGCGGCACCAACGCCACCACTACCACTGC	2384		
Db	613	GACACACACAAACAAACGACACAAACAAACAACTACTACAACTACTACCCTACTACTAC	672		
Qy	2385	ATCAAGGATTAAGTGCCTCCCATCTGTCGCAAAATTTCTGGGGCAGGAGAGCTTTTGACAAGACGGG	2444		
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RESULT 15

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US-08-928-361B-2
: Sequence 2, Application US/08928361B
: Patent No. 6071518
: GENERAL INFORMATION:
: APPLICANT: Petersen, Carolyn
: TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
: TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS ANALOGS AND FRAGMENTS
: TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
: TITLE OF INVENTION: SPECIES INFECTIONS
: NUMBER OF SEQUENCES: 30
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: PETERS, VERNY, JONES & BIKSA
: STREET: 385 Sherman Avenue, Suite 6
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94306-1840
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/928,361B
: FILING DATE: 12-SEP-1997
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/026,062
: FILING DATE: 13-SEP-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Verny, Hana
: REGISTRATION NUMBER: 30,518
: REFERENCE/DOCKET NUMBER: 480.76-1(HV)
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650-324-1677
: TELEFAX: 650-324-1678
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5511 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
US-08-928-361B-2

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[illegible]

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 27, 2002, 00:20:19 ; Search time 181 Seconds
(without alignments)
12981.546 Million cell updates/sec

Title: US-09-919-770-3
Perfect score: 5784
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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 363474 seqs, 203117208 residues

Total number of hits satisfying chosen parameters: 726948

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications, NA.*

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
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- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	3573.6	61.8	3596	10	US-09-822-682-1
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6	1548.8	26.8	7231	10	US-09-919-172-64
7	1529.8	26.4	5830	10	US-09-925-301-205
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9	601.6	10.4	2439	9	US-09-954-531-359
c 10	595.6	10.3	619	9	US-09-925-380-327
c 11	595.6	10.3	619	10	US-09-922-217-327
c 12	595.6	10.3	619	10	US-09-833-263-327
c 13	540.2	9.3	637	10	US-09-815-343-1448
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c 17	423.6	7.3	435	9	US-09-736-457-592
c 18	423.6	7.3	435	9	US-09-902-941-592
c 19	423.6	7.3	435	10	US-09-902-941-592
c 20	423.6	7.3	435	10	US-09-604-287A-223

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c 22	370	6.4	478	10	US-09-815-343-834	Sequence 834, App
23	335.4	5.8	486	10	US-09-925-299-478	Sequence 478, App
24	332.2	5.7	438	10	US-09-833-381-1864	Sequence 1864, App
c 25	319.6	5.5	390	10	US-09-954-456-785	Sequence 785, App
c 26	319.6	5.5	390	10	US-09-880-107-1916	Sequence 1916, App
c 27	300	5.2	300	10	US-09-815-343-508	Sequence 508, App
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c 33	104.2	1.8	390	10	US-09-790-399-7	Sequence 7, Appli
c 34	100.6	1.7	312	9	US-09-736-457-952	Sequence 952, App
c 35	100.6	1.7	312	9	US-09-902-941-952	Sequence 952, App
c 36	98.8	1.7	406	10	US-09-960-352-8997	Sequence 8997, App
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c 40	91.2	1.6	408	10	US-09-960-352-7596	Sequence 56, Appl
c 41	89.6	1.5	392	10	US-09-960-352-260	Sequence 7596, App
c 42	89.6	1.5	439	10	US-09-960-352-3062	Sequence 3062, App
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c 44	88	1.5	2820	10	US-09-854-845-15	Sequence 15, Appl
45	88	1.5	2865	10	US-09-854-845-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1

US-09-919-770-3

Sequence 3, Application US/09919770

Patent No. US20020048577A1

GENERAL INFORMATION:

APPLICANT: Bornstein, Paul

APPLICANT: Kyriakides, Themis

APPLICANT: Ratner, Buddy

APPLICANT: Glachelli, Cecilia

APPLICANT: Martinson, Laura

APPLICANT: Scatena, Marta

TITLE OF INVENTION: Methods and Devices to Modulate the Wound Response

FILE REFERENCE: UOFW117618

CURRENT APPLICATION NUMBER: US/09/919,770

PRIOR FILING DATE: 2001-07-31

PRIOR APPLICATION NUMBER: US 60/222,071

PRIOR FILING DATE: 2000-08-01

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn version 3.0

SEQ ID NO 3

LENGTH: 5784

TYPE: DNA

ORGANISM: Homo Sapien

FEATURE:

NAME/KEY: CDS

LOCATION: (240)..(3755)

US-09-919-770-3

Query Match 100.0%; Score 5784; DB 10; Length 5784;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5784; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ACGGCATCAAGCCGCGCTGGCCCGGAGCCGCTGGCCACGTCACAGCCCTGCACAGAGAG 60

Qy 61 CGGCATATAAAGCCGCGCTGGCCCGGAGCCGCTGGCCACGTCACAGCCCTGCACAGAGAG 120

Db 61 CGGCATATAAAGCCGCGCTGGCCCGGAGCCGCTGGCCACGTCACAGCCCTGCACAGAGAG 120

Qy 121 CTGAGGCCGCGGTCTCTCGCTCCAGCAGAGCTGGCGCTTCTGACTCGGTCCGGAACAC 180

Db 121 CTGAGGCCGCGGTCTCTCGCTCCAGCAGAGCTGGCGCTTCTGACTCGGTCCGGAACAC 180

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Qy	2461	ATGATGACGATGACAAATGACGSGTGTGACCGATGAGAAGACAACCTGCCAGCTCCTCTTCA	2520
Db	2461	ATGATGACGATGACAAATGACGSGTGTGACCGATGAGAAGACAACCTGCCAGCTCCTCTTCA	2520
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Db	2521	ATCCCGCCAGGCTGACTATGACAAAGGATGAGTTTGGGAGCCGCTGTGACAACTGCOCCT	2580
Qy	2581	ACGTGCACAACCTGCCAGATCGCACAGACAACAATGGAGAGGGTGAAGCCTGCTCCG	2640
Db	2581	ACGTGCACAACCTGCCAGATCGCACAGACAACAATGGAGAGGGTGAAGCCTGCTCCG	2640
Qy	2641	TGGACATTTGATGGGGACGATGCTTCTCAATGAACGAGACAATTTGCCCTACGCTTACAACA	2700
Db	2641	TGGACATTTGATGGGGACGATGCTTCTCAATGAACGAGACAATTTGCCCTACGCTTACAACA	2700
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RESULT 2

US-09-880-107-2160
 ; Sequence 2160, Application US/09880107
 ; Patent No. US20020142981A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Horne, Darci T.
 ; APPLICANT: Vockley, Joseph G.
 ; APPLICANT: Scherf, Uwe
 ; APPLICANT: Gene Logic, Inc.
 ; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
 ; FILE REFERENCE: 44921-5028-WO
 ; CURRENT APPLICATION NUMBER: US/09/880,107
 ; CURRENT FILING DATE: 2001-06-14
 ; PRIOR APPLICATION NUMBER: US 60/211,379
 ; PRIOR FILING DATE: 2000-06-14
 ; PRIOR APPLICATION NUMBER: US 60/237,054
 ; PRIOR FILING DATE: 2000-10-02
 ; NUMBER OF SEQ ID NOS: 3950
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2160
 ; LENGTH: 5784
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 L12350
 US-09-880-107-2160

Query Match 100.0%; Score 5784; DB 10; Length 5784;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 5784; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 ACGGCATCCAGTACAGAGGGGCTGGACTTGGACCCCTGCAGCAGCCCTGCACAGGAGAAG 60
 Qy 61 CGGCATATAAAGCGCGCTGCCGGAGCCGCTCGGCCACGCTCCACCGGAGCATCTGCA 120
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QY 481 AGGAGGCTTCTTCTCCTCACGCGCCAGCTCAAGCAGGACGCGCAAGTCCAGGGGACAGCTGT 540
Db 481 AGGAGGCTTCTTCTCCTCACGCGCCAGCTCAAGCAGGACGCGCAAGTCCAGGGGACAGCTGT 540
QY 541 TGGCTCTGGAGGGCCCCGGTCTCTCCAGAGGAGTTCGAGATGGTCTCCAAAGCGCCCCG 600
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RESULT 4

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US-09-822-682-1
: Sequence 1, Application US/09822682
: Patent No. US2002011921A1
: GENERAL INFORMATION:
: APPLICANT: Detmar, Michael J.
: APPLICANT: Streit, Michael
: TITLE OF INVENTION: THROMBOSPONDIN-2 AND USES THEREOF
: FILE REFERENCE: 10287-01002
: CURRENT APPLICATION NUMBER: US/09/822,682
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: CURRENT FILING DATE: 2001-03-30
: PRIOR APPLICATION NUMBER: 09/536,087
: PRIOR FILING DATE: 2000-03-24
: PRIOR APPLICATION NUMBER: 60/127,221
: PRIOR FILING DATE: 1999-03-31
: NUMBER OF SEQ ID NOS: 11
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 3596
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (26)...(3541)
US-09-822-682-1

Query Match 61.8%; Score 3573.6; DB 10; Length 3596;
Best Local Similarity 99.68; Pred. No. 0;
Matches 3582; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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QY 2135 CGGGGTGCGCCTGGAAGCAGCCAAAGCAGAAAGTGTGTGAGCCGGAACCCATG 2194
Db 1921 CGGGGTGCGCCTGGAAGCAGCCAAAGCAGAAAGTGTGTGAGCCGGAACCCATG 1980
QY 2195 CAAGNCAAGACACACAACTGCCAAGCAGCGGGAGTGCATCTACCTGGGTCACTTCAG 2254
Db 1981 CAAGGACAAGACACAACTGCCAAGCAGCGGAGTGCATCTACCTGGGCACCTTCAG 2040
QY 2255 CCACCCCATGTAAAGTGGAGTGGCAGACAGCTACGGGGGAGGGCTCATCTGCCG 2314
Db 2041 CGACCCCATGTAAAGTGGAGTGGCAGAGGCTACGGGGGAGGGCTCATCTGCCG 2100
QY 2315 GGAGGACTCGGACCTGGACGCTGGCCCAACCTCAATCTGTGCTGCGCCACCAAGCCAC 2374
Db 2101 GGAGGACTCGGACCTGGAGGCTGGCCCAACCTCAATCTGTGCTGCGCCACCAAGCCAC 2160
QY 2375 CTACCACTGCATCAAGGATTAATCTGCCCCCATCTGCCAAATCTTGGCAGGAAGACTTGA 2434
Db 2161 CTACCACTGCATCAAGGATTAATCTGCCCCCATCTGCCAAATCTTGGCAGGAAGACTTGA 2220
QY 2435 CAAGGACGGGATTTGGGATGCTGTGATGATCAGCATGACAATGACGGTGCACCGATCA 2494
Db 2221 CAAGGACGGGATTTGGGATGCTGTGATGATCAGCATGACAATGACGGTGCACCGATCA 2280
QY 2495 GAAGGACAACCTGCCAGCTCTCTTCAATCCCGCCGAGGTGACTATGACAAGGATGAGT 2554
Db 2281 GAAGGACAACCTGCCAGCTCTCTTCAATCCCGCCGAGGTGACTATGACAAGGATGAGT 2340
QY 2555 TGGGACCGCTGTGACAACTGCCCTTACGTGCACAACCTGCCAGATGCCAGACAGACAA 2614
Db 2341 TGGGACCGCTGTGACAACTGCCCTTACGTGCACAACCTGCCAGATGCCAGACAGACAA 2400
QY 2615 CAATGGAGAGGTGACGCTGCTCGTGACATTTGATGGGACGATGCTTCAATGAAG 2674
Db 2401 CAATGGAGAGGTGACGCTGCTCGTGACATTTGATGGGACGATGCTTCAATGAAG 2460
QY 2675 AGACAATTTCCCTACGCTTACAACACTGACAGAGGACACGGATGTGACGGTGTGG 2734
Db 2461 AGACAATTTCCCTACGCTTACAACACTGACAGAGGACACGGATGTGACGGTGTGG 2520
QY 2735 GGATCAGTGTGACAACTGCCCTTGGTGCACAACCTTGCACAGACCGAGTGGACAATGA 2794
Db 2521 GGATCAGTGTGACAACTGCCCTTGGTGCACAACCTTGCACAGACCGAGTGGACAATGA 2580
QY 2795 CTTTCTTTGGGGACCACTGTGACAACAGGACATAGATGACGACGGCCACCAAGACAA 2854
Db 2581 CTTTCTTTGGGGACCACTGTGACAACAGGACATAGATGACGACGGCCACCAAGACAA 2640
QY 2855 CCAGGACAACCTGCCCTTACATCTCCAACGCCAACCAAGCTGACCATGACAGAGCGGCA 2914
Db 2641 CCAGGACAACCTGCCCTTACATCTCCAACGCCAACCAAGCTGACCATGACAGAGCGGCA 2700
QY 2915 GGGCCACGCTGTGACCTGTGATGATGACAACGATGGCTGCCCGATGACAGGGAACCTG 2974
Db 2701 GGGCCACGCTGTGACCTGTGATGATGACAACGATGGCTGCCCGATGACAGGGAACCTG 2760
QY 2975 CGGGTCTGTCTTCAACCCAGACAGGAGCTTGGACGGTGTGACGGGTGATATTG 3034
Db 2761 CGGGTCTGTCTTCAACCCAGACAGGAGCTTGGACGGTGTGATGACGGGTGATATTG 2820
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Db 2821 TAAAGATGATTTGACAATGACAACATCCAGATATTGATGATGTGTCTTGAATAACAA 2880
QY 3095 TGCCATCAGTGAAGACAGCTTCAGGAACCTTCAGATGTCTCCCTTGGATCCCAAGGGAC 3154
Db 2881 TGCCATCAGTGAAGACAGCTTCAGGAACCTTCAGATGTCTCCCTTGGATCCCAAGGGAC 2940
QY 3155 CACCCAAATTTGATCCCAACTGGGTGCTTCCGATCAAGGCAAGGAGCTGGTTTCACAGAC 3214
Db 2941 CACCCAAATTTGATCCCAACTGGGTGCTTCCGATCAAGGCAAGGAGCTGGTTTCACAGAC 3000


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Qy 3546 GCCTGGGAAGGACTACACGGCCTATAGGTGGACCTGACTACAGGCCCAAGACCGGCTAC 3605
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Qy 3606 ATCAGAGCTTAGTGCATGAAGGAACACAGGTCACTGGCAGACTCAGGACCTATCTATCAGC 3665
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Qy 3666 CAACACTACGCTGGCGGGCGGCTGGGTCTATTGTCTTCTCTCAAGAAATGCTCTATTTC 3725
Dy 3532 AAAACCTATGCTGGTGGTAGACTAGGGTGTGTTGTCTCTCAAGAAATGGTGTCTTC 3591
Qy 3726 TCAGACCTCAAGTACGAGTACAGAGATATTTAAACAAGATTTGCTGCAAT 3775
Dy 3592 TCTGACCTGAAATACGAATGAGAGATCCCTAATCATCAAAATTTGTGAT 3641

RESULT 6
US-09-919-172-64
; Sequence 64, Application US/09919172
; Patent No. US20020119463A1
; GENERAL INFORMATION:
; APPLICANT: Paris, Mary
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 64
; LENGTH: 7231
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020119463A1 1399366.20
; NAME/KEY: unsure
; LOCATION: 5601, 5609, 7107
; OTHER INFORMATION: a, t, c, g, or other
US-09-919-172-64

Query Match 26.8%; Score 1548.8; DB 10; Length 7231;
Best Local Similarity 65.9%; Pred. No. 0;
Matches 2325; Conservative 0; Mismatches 1172; Indels 33; Gaps 4;

Qy 252 CTGGTCTGCTGGCTCTGCTGGTGGCGCCAGCAGCGCAAGCTGGTCAACAGGACAAAGAC 311
Dy 197 CTGTTCTCTGATGCATGTGTGGCACCACCGCATTCAGAGTCTGGCGGAGACA---AC 253
Qy 312 ACGACCTTCGACCTTTTCAGTATCAGCAACATCAACCCGCAAGACCATTTGGCGCCAGCAG 371
Dy 254 ACGGTGTTTGACATCTTTGAACTACCGGGCGCGCCCAAGGGTCTGGCGCGCAGCTG 313
Qy 372 TTCGCGCGCGCGCGCCCGGGTGGCGGCTTACCGCTTCGTCGCGCTTTGACTACATCCCA 431
Dy 314 GTGAAGGCGCGCGACCCCTTCAGGCCACGCTTTCGCGCATCGAGGATGCCAACCTGATCCCC 373
Qy 432 CGGTGAACCGAGATGACCTTCAGCAAGATCAACCAAGATCATGCGCGCAGAAGAGGGCTTC 491
Dy 374 CCTGTGCTGATGACAAGTTCGAAGNCTTCCAGNCTTGGTGGATGCTGTGCGGGCAGAAAGGGTTTC 433
Qy 492 TTCCTCAGCGCCCGCTCAACGAGCAGCGCAAGTCCAGGGGCACGCTGTTGGCTCTGAGC 551
Dy 434 CTCCTTCGGCATCCCTCAGGCGAGATGAAGAACCCCGGGGCGACGCTGTGGCCCTGGAG 493
Qy 552 GGGCCCGGCTCTCCAGAGGCGAGTTCGAGATCGTCTCAACGGGCGCGCGGACACGCTG 611
Dy 494 CGGAAGACCACTCTGGGCCAGGCTTTCAGCGTGGTGTCCATGCGCAAGCGGGCACCCCTG 553
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Qy 612 GATCTCAGCTACTGATGTGACGGCACCCCGGCGATGTGGTCTCCCTTGGAGGACGCTCGGCCGTG 671
Dy 554 GACCTCAGCCTGACCGTCCAAAGAAAGCAGCAGCTGGTGTCTGTGGAAGAGCTCTCCTG 613
Qy 672 GCTGACTCGCAGTGAAGAACGTCACCGTGCAGGTGGCTGGCGAGACCTACAGCTTGCAC 731
Dy 614 GCAACCGCCAGTGGAGAGCATCACCTGTTTGTGAGGAAGCAGGCGCCAGCTGTAC 673
Qy 732 GTGGCTCGACCTCATAGGACCACTGCTCTGGACGAGCCCTCTACGAGCACCTGCAG 791
Dy 674 ATCGACTGTGAAAGATGAGAAATGCTGAGTTGGAGCTCCCATCCAAAGGCTCTTACC 733
Qy 792 GCGNAAGACGCGGATGTCGTGGCCAAAGCTC-----TGCAGAGAGAGTCACTTC 845
Dy 734 AGAGACCTGGCCAGCATCGCAGACTCCGATCGCAAAAGGGGGGCGTCAATGACAATTC 793
Qy 846 AGGGTTTTGCTTCAGAACGTCACCTAGTGTGTTGAAACTCTGTGGAAGATATTCTAAGC 905
Dy 794 CAGGGGTGCTGCAGATGTGAGGTTTGTCTTTGGAACCAACACAGAAAGACATCTCAG 853
Qy 906 AAGAAGGTTTGCACAGCAAGGCCAGGAGCTGAGATCAACGCCATCAGTGAGAACACAG 965
Dy 854 AACAAAGGCTGC-----TCCAGCTCTACAGTGTCTCTCACCTTTGACAAACAACGTG 907
Qy 966 ACGTGGCCCTGGTCCGATGTCAACACGAGTACGTGGGCCCCAGCTCGGAGAGAGG 1025
Dy 908 GTGAATGTTCCAGCCCTGCCATCGCAGCTAACTACATTTGGCCACAAGAACAGACTTG 967
Qy 1026 CCCGAGGTGCGAACACGCTGTCGCGAGGAGTGGGAAACATGTCACGAGCTCTCGGG 1085
Dy 968 CAAGCCATCTCGGCATCTCTGTGTGATGAGCTGTCCAGCATGGTCTGGAACCTCAGGGGC 1027
Qy 1086 CTCACAGCTCTCGTGAACACGCTCAGCGAGAACCTCAAGAGAGTGTGCAATGATACAC 1145
Dy 1028 CTGCGACCATTTGTGACCAACGCTGCAGCAGCAGCTCCGCAAGTACTCAAGAGAACAA 1087
Qy 1146 TTTCTCTGGGAGCTCATTTGGTGGCCCTCTTAAGACAAGAACATGTCAGTCTTGGGAG 1205
Dy 1088 GAGTTGGCCAAATGAGCTGAGCGCGCTC-----CCCTATGCTATCAC 1129
Qy 1206 GATGCCCGTTCTTTGCGGAAATGAACGTGGGTGGAGAGCTGCACAGCTGCACACGTGAC 1265
Dy 1130 AACGAGTTCAGTACAGAAATAACGAGGAATGGACTGTTGATAGCTGCAGTGTGCAC 1189
Qy 1266 TGCAGAAATTTAAACCAATTTGCCACCAATCACTGCCCGCTGCAACCTCGCCCACT 1325
Dy 1190 TGTCAAGACTCAGTTTACCATTCTGCAAAAAGGTGTCTTGCCTCCATCATGCTCTCCTCA 1249
Qy 1326 CCATCTTTTGGAGAGGCGAATGCTGCGCTTCTCTGCTCCACTCGGTGGAGCGTGAAGAG 1385
Dy 1250 GCCACAGTCTCTGATGGAGATGCTGCTGCTGCTTGGCCCGCAGGACTCTGCGGACGAT 1309
Qy 1386 GGCTGCTCTCGTGGGAGAGTGGACCCAGTCTCCGTGACGTGGCTCTGGGACCCAG 1445
Dy 1310 GCTGGTCTCATGTCGTCGAGTGGACCTCTCTGTTTACGAGCTGTGGCAATGGAATTCAG 1369
Qy 1446 CAGAGAGCCGCTCTGTGAGCTCACCAGCAACACTGCTTGGGCGCTTCGATCCAGACA 1505
Dy 1370 CAGCGCGCGCTCTCTGATACGCTCAACACCCATGAGAGGCTCTCTGCTCCAGACA 1429
Qy 1506 CGGGTTCGAGTCTCAGCAAGTGTGACACCCGATCCCGCAGAGCGGGCTGGAGCCAC 1565
Dy 1430 CGGACTGCCACATTCAGGAGTGTGACAAGATTTAAACAGGATGGTGGCTGGAGCCAC 1489
Qy 1566 TGGTCACTTGGTCTCTGATGCTGTGACCTGTGGAGTGGCAATATCACAGCATCCGT 1625
Dy 1490 TGGTCCCCGTGCTCATCTGTTCTGTGACATGTTGTGTGATGGTGTGATCACAGGATCCGG 1549
Qy 1626 CTCTCAACTCCCAAGTGGCCAGATGGGGGCAAGAAATTCGAAAGGAGTGGCGGGAG 1685
Dy 1550 CTCTGCACTCTCCCGACCCCGCAGATGACGGGAACCTCTGTGAAGGCGAAGCGGGAG 1609
Qy 1686 ACCAAAGCTGCCAGGGGCGCCCATGCCCAATTCGATGGCCGCTGGAGCCCTTGGTCCCG 1745
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Db	1610	ACCAAAGCTGCAGAAGAAGACGCGCTGCCCATCAATGAGAGGTGGGGTCTTGGTGCACCA	1669
Qy	1746	TGGTGGCGCTGCACCTGTGCGGTGGGATCCGGGAGCGCACCCGGGTCTGCAAC	1805
Db	1670	TGGGACATCTGTTCTGTCACCTGTGGAGGAGGGGTACAGAACTAGTCTCTGTCAC	1729
Qy	1806	AGCCCTGAGCCTCAGTACGGAGGAAGGCGCTGCGTGGGGGATGTGCAGAGCGTCAGATG	1865
Db	1730	AACCCACACCCAGTTTGGAGCAAGGACTGCGTTGGTGTATGTAACAGAAACACAGATC	1789
Qy	1866	TGCAACAAGAGGAGCTGCCCGTGGATGCGTGTATTCCAAACCCCTGCTCCGGGAGCC	1925
Db	1790	TGCACAAGCAGGACTGTCCAATTGATGATGCGCTGTCCAATCCCTGCTTTCGCCGGCGTG	1849
Qy	1926	CAGTGCAGCAGCTTCCCGATGGGTCCCTGGTTCATGCGGGCTTCTGCCCTGTGGGTCTCTTG	1985
Db	1850	AAGTGTACTAGCTACCGTGTATGCGACTGGAATGTGTGCTTGTCCCTCGTTACAGT	1909
Qy	1986	GGCAATGGCACCCACTGTGAGGACCTTGGAGCTGTGCCCTGGTCCCGGACATCTGCTTC	2045
Db	1910	GGAAATGGCATCCAGTGCACAGATGTTGATGAGTGCAAAAGATGCGCTGATGCGCTGCTC	1969
Qy	2046	TCCACACGAAAGTGGCTTCGCTGTGTCAACTACAGCTTACGCTTGGTTCACATGCGCTGCCCTGC	2105
Db	1970	AACCACAATGGAGGAGCCGGTGTGAGAACACGGGACCCGGCTACAACTGCGCTGCCCTGC	2029
Qy	2106	CCGCCCGATACAGAGGAACAGCCCGTGGGGTTCGGCTTGGAGAGACCAAGACAGGAA	2165
Db	2030	CCCCACGCTTACCGGCTACAGGCCCTTCGCGCAGGGTGTGCAACATGTGCCACGGCCAAC	2089
Qy	2166	AAGCAAGTGTGTGAGCGCGAAACCCATGCAAGGAGCAAGACACACACTGCCACAAGCAC	2225
Db	2090	AAACAGTGTGCAAGCCCCGTAAACCCCTGCACGGATGGGACCCAGCACTGCAACAAGAAC	2149
Qy	2226	CGGAGTGCATCTACCTGGGTCACTTCACGACCCCATGTATCAAGTGGAGTGCACAGACA	2285
Db	2150	GCCAAGTGCAACTACCTGGGCCACTATACGACCCCATGTACCCGTGCGAGTGCACAGCCT	2209
Qy	2286	GGCTTACGCGGGCACGGGCTCATCTGCGGGGAGGACTCGGACCTTGGAGCGTGGCCCCAAC	2345
Db	2210	GGCTACGCTGGCAATGGCATCATCTGCGGGGAGGACAGACCTTGGATGGCTGGCCCCAAT	2269
Qy	2346	CTCAATCTGGTCTGCGCCACCACCGCCACTACCACTGCATCAAGGATAACTGCCCCCAT	2405
Db	2270	GAGAACCTGGTGTGCGTGGCCAAATCGACTTACCCTGCAAAAGGATAATTGGCCCCAAC	2329
Qy	2406	CTGCCAAATCTGGGAGAGAGACTTTGACAGGAGCGGATTTGGGATGCGCTGTGATGAT	2465
Db	2330	CTTCCCAACTCAGGGCAGGAAGACTATGACAAGGATGGAATTGGTGTGATGCGCTGTGATGAT	2389
Qy	2466	GAGGATGACAATACGSGTGTGCCGATGAGAGGACAACGCCAGCTCCCTCTTCAATCCC	2525
Db	2390	GAGATGACAATGATAAATTCGACATGACGGGACAACGTGCCATTCCATTACACCCA	2449
Qy	2526	CGCCAGGCTGACTATGACAAAGATGAGGTGGGGACCGCTGTGACAACGTGCCCTTACGTG	2585
Db	2450	GCTCAGTATGACTATGACAGAGATGATGTGGAGACCGCTGTGACAACGTGCCCTTACAC	2509
Qy	2586	CACAACCCCTGCCAGATCGACACAGACAACAATGGAGAGGTGACGCTGCTCCGTGGAC	2645
Db	2510	CACAACCCAGATCAGGCACACACAGACAACAATGGGAAGGAGACGCGTGTGCTGCACAG	2569
Qy	2646	ATTGATGGGACGATGCTTCAATCAACAGACACAATTTGCTCCCTAGGTCTACACACTGAC	2705
Db	2570	ATTGATGGAGAGGATATCTCAATGAACGGGACAACGCCAGTAGCTCTCAATTTGGAC	2629
Qy	2706	CAGAGGACACCGATGGTGACGGTGTGGGGATCACTGTGACAACCTGCCCTTGGTGCAC	2765
Db	2630	CAGAGACACTGATATGATGGGTTTGGAGATCAGTGTGACAATTTGCCCTTTGGAACAC	2689
Qy	2766	AACCCCTGACCACGACGCTGGACAATGACCTTGTGGGGACCACTGCTGACAACAACGAG	2825

Db	2630	AATCCGGATCAGCTGGACTCTGACTCAGACCGGATTTGGAGATACCTGTGACAACAATCAG	27419
Qy	2826	GACATAGATGACGACGGCCACCAAGAACACACAGGACAAGCTGCCCTACATCTCCAAGGCC	28855
Db	2750	GATATTGATGAAGATGCCACAGACAATCTGGACAACCTGTCCCTATGTGCCCAATGCC	2809
Qy	2886	AACCAAGGTGACCATGACAGAGACAGCGCCAGGGGAGCGCTGTGACCCCTGTGATGACAAAC	2945
Db	2810	AACCAAGGTGACCATGACAAAGATGGCAAGGGAGATGCCGTGTGACCAAGCATGATGACAAC	2869
Qy	2946	GATGGCTGCCGATGACAGGGACAACCTGCCGCTGTGTCTCAACCCAGACACGAGGAC	3005
Db	2870	GATGGCATCTCTGATGAAGAGCAACTGCAGCTGTGCCCAATTCGCCGACCAAGGAC	2929
Qy	3006	TTGGACGGTGATGACAGGGGTGATATTTGTAAAGATGATTTTGACAATGACAACATCCCA	3065
Db	2930	TCTGACGGCATGCTGAGGTGATGCCCTGCAAGATGATTTTGACCATGACAGTGTGCCA	2989
Qy	3066	GATATTGATGATGTGTCTCTGAAACAAATGCCATCTCAGTGAGACAGACTTCAGGAATTC	3125
Db	2990	GACATCATGACATCTGTCTCTGAGAAATGTGTGATCATGCTGAGACCGCACTTCGCCGATTC	3049
Qy	3126	CAGATGTGCCCTTGATGATCCAAAGGACCAACCCAAATTTGATCCCACTGGTCTATTCGC	3185
Db	3050	CAGATGATCTCTGAGCCCAAGGGACATCCCAAAATGACCTTAATCGGGTGTGACG	3109
Qy	3186	CATCAAGGCAAGAGCTGGTTTCAGACAGCCAACCTCGGACCCCGGCATCGCTGTAGTTTT	3245
Db	3110	CATCAGGCTAAAGCACTCGTCCAGACTGTCAACTCTGATCCTTGGACTCGCTGTAGTTAT	3169
Qy	3246	GACGAGTTTGGGTCTGTGGACTTCAGTGGCACTTCTTACGTAAACATGACGCGGAGCAC	3305
Db	3170	GATCAGTTTAAATGCTGTGGACTTCAGTGGCACTTCTTCTATCAACACCGCAAGGAGCAT	3229
Qy	3306	GACTATCTGGCTTCGTTCTTTGGTTTACCAGTCAAGCAGCGCTTCTATGTGGTCACTGG	3365
Db	3230	GACTATCTGGATTGTCTTTGGCTACCACTCCAGCGCGCTTTATGTGTGATGTGG	3289
Qy	3366	AAGCAGTGTACGACAGACTACTGGGAGGACACAGCCACCGGGGCTATPGCTACTCCGGC	3425
Db	3290	AAGCAAGTCAACCCAGTCTCTACTGGGACACCAACCCAGAGGGCTCAGGGATACTCGGC	3349
Qy	3426	GTGTCCCTCAAGTGTGAACTCCACACGGGAGCGGGGAGCACTGTAGGAACGCGCTG	3485
Db	3350	CTTTCTGTGAAGTTGTAACTCCACACAGGGCTGCGGAGCACTTCGGGAAGCGCCTG	3409
Qy	3486	TGGCACACGGGGAACACCGCGGCGAGGTGCGAACTTTATGGCACGACCCCAAGAACTT	3545
Db	3410	TGGCACACAGGAACACCCCTGCCAGGTGCGCACCTCTGGCATGACCTCGTCACATA	3469
Qy	3546	GGCTGGAAGGACTACAGCGCTTATAGTGGGCACTGTGACTCACAGGCCAAGACCGGTAC	3605
Db	3470	GGCTGGAAGATTTTCAACGCCCTACAGTGGCTCTTCACCCACAGGCCCAAGACGGTTTC	3529
Qy	3606	ATCAGAGTCTTACTGCACTGAAGGAAACAGGTCATGGCAGACTCAGGACCTATCTATGAC	3665
Db	3530	ATTAGTGGTGATGATGAAGGGAAGAAATCATGGCTGACTCAGGACCCATCTATGAT	3589
Qy	3666	CAAACTTACGCTGGCGGGGCTGGGTCTATTGTGTTCTTCTCAAGAAATGGTCTATTTTC	3725
Db	3590	AAAACCTATGCTGGTGTAGACTAGGTTGTTGTCTTCTCTCAAGAAATGGTGTCTTC	3649
Qy	3726	TCAGACCTCAAGTACGAATTCAGAGATATTTTAAACAAGATTTGCTGCATTT	3775
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RESULT 7
US-09-925-301-205
; Sequence 205, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.

;; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

;; FILE REFERENCE: PA106

;; CURRENT APPLICATION NUMBER: US/09/925,301

;; CURRENT FILING DATE: 2001-08-10

;; PRIOR APPLICATION NUMBER: PCT/US00/05882

;; PRIOR FILING DATE: 2000-03-08

;; PRIOR APPLICATION NUMBER: 60/124,270

;; PRIOR FILING DATE: 1999-03-12

;; NUMBER OF SEQ ID NOS: 1694

;; SOFTWARE: PatentIn Ver. 2.0

;; SEQ ID NO 205

;; LENGTH: 5830

;; TYPE: DNA

;; ORGANISM: Homo sapiens

;; FEATURE:

;; NAME/KEY: misc_feature

;; LOCATION: (5584)

;; OTHER INFORMATION: n equals a,t,g, or c

;; NAME/KEY: misc_feature

;; LOCATION: (5585)

;; OTHER INFORMATION: n equals a,t,g, or c

;; NAME/KEY: misc_feature

;; LOCATION: (5821)

;; OTHER INFORMATION: n equals a,t,g, or c

;; US-09-925-301-205

Query Match 26.4%; Score 1529.8; DB 10; Length 5830;
Best Local Similarity 65.8%; Pred. No. 0;
Matches 2325; Conservative 2; Mismatches 1169; Indels 35; Gaps 6;

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QY 187 CTGTTCTGTATGATGTGTGGCACCACACCGCATTCAGAGTCTGGCGGAGACA---AC 243
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 312 ACGACCTTCGACCTTTTCAGTATCAGCAACATCAACCGCAGACCATTTGGCGCCAAAGCAG 371
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 244 AGCGTGTGTGACATCTTGAACATCACCGGGCCGCCGCAAGGGTCTGGCGCCGACTG 303
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 372 TTCGGGGGCCCGACCGCGGGTCCGGCTTACCGTTTACCGTTTGGCGCTTTGACTACATCCCA 431
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 304 GTGAAGGGCCCCCGCTTCAGCCCAAGCTTTCGGCATCGAGGATGCCAACCTGATCCCC 363
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 432 CCGGTGAACGCAGATGACCTCAGCAAGATCACCAGATCATCGCGCAGAGGAGGCTTC 491
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 364 CCTGTGCTGTATGACAGTTCACAGACCTGTGTGATGCTGTGGCGGAGAAAAGGTTTC 423
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 492 TTCCTCAGCGCCCGCAGCAAGTCCAGGGCAGCGCTTTGGCTCTGGAG 551
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 424 CTCCTTCTGGCATCCCTGAGGCAGATGAAGAAGACCCGGGCAGCTGCTGGCCCTGGAG 483
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 552 GGCCCCGGTCTCTCCAGAGCAGTTTGGAGATCTCTCCAACGGCCCCCGGACACGGTG 611
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 484 CGAAAGAACCATCTTGGCCAGCTTTCAGCGTGTGTCCATGATGCAAGGGCGGACCCCTG 543
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 612 GATCTACCTACTGATTTAGCGGCACCGGCATGTGCTCTCCCTGGAGGAGCTGGGCTG 671
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QY 544 GACCTACCTTACCGTCCAAAGAAACAGCACGCTGTGTGTGGGAAGAGCTCTCCCTG 603
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QY 672 GCTCACTTCGAGTGAAGAGCTCACCGTGCAGGTGGCTGGCGAGACCTACAGCTTTGCAC 731
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 604 GCAACCGGCAGTGAAGAGCATCACCTGTTTGTGCAGGAAGACAGGGCCAGCTGTAC 663
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QY 732 GTGGGCTGGACCTCATTAGGACACAGTTGCTCTGGACGAGCCCTTCTACGAGCACCTGCAG 791
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 664 ATCGACTGTGAAGATGGAGATGCTGAGTTGGACGTCCCATCCCAAGGGCTTCAACC 723
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 792 GCGAAAGAGCCGGATGAGTGGCCAAAGGCTC-----TGCCAGAGAGTCACTTC 845
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 724 AGACCTTGGCCAGCATCGCCAGACTCCGCATCGCAAGGGGGCGTCAATGACAATTC 783
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 846 AGGGGTTTGTTCAGAACCTCCACCTAGTGTGTTTCAAACTCTGTGGGAAGATATTCTAAGC 905
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 784 CAGGGGCTGCTGACAGATGTGAGGTTTGTCTTGGACCAACACACAGAGACATCCTCAGG 843
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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QY 906 AAGAAGGGTTGCCAGCAAGGCCAGGGAGCTGAGATATCAAGCCCATCATGATGAGAACAACAGAG 965
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 844 AACAAAGGCTGC-----TCCAGCTCTACCAAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 897
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 966 ACGCTGCGCCCTGGTGGTCCGATGTCCACACCGAGTACGTGGGCCCCCAGCTGGGAGAGGAGG 1025
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 898 GTGAATGGTTCCAGCCCTGCCATCCGACATTAACATACATTTGGCCCAAGAACAAAGACTTGG 957
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1026 CCCGAGGTGTCCGAACGCTCTGTCGAGGAGCTGGGAAACATGGTCCAGGAGCTCTCCGGGG 1085
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 958 CAAGCCATCTGCGCATCTCTCTGTGATGAGCTGTCCAGCATGGTCTTGGAACTCAGGGGC 1017
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1086 CTCACAGTCTCTGTGAACAGCTCAGCGAGAACCTCAAGAGAGTGTGCAATGATACACAG 1145
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1018 CTGCGCACCAATTTGTAGCCACGCTCGAGGACAGCATCCGCAAGTGAAGAGAGACAAA 1077
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1146 TTTCTCTGGGAGCTCATTGGTGGCCCTCTTAAGACAAGGAACATGTTCAGCTTGTCTGGCAG 1205
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1078 GAGTTGGCAATGAGCTGAGCGGCCCTC-----CCCTATGCTATCAC 1119
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QY 1206 GATGGCCGGTTCTTTTGGGAAATGAACAGTGGTGGTGGACAGCTGCACACCTGTACCC 1265
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QY 1120 AACGAGTTTCAGTACAGAAATAACAGGAATGGACTGTGTATAGCTGCACCTGAGTGTAC 1179
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1266 TGAAGAAATTTAAACACATTTGGCCACCAATACCTGCCCGCTGCACCTGCCAGT 1325
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QY 1180 TGTGAGAACTCAGTTACCATCTGCAAAAAGGTCTCTGCCCATCATGCCCTGTCTCCAAT 1239
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QY 1326 CCATCTCTTGTGGAAGCGAATGCTGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1385
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QY 1240 GCCACAGTCTGTATGAGAAATGCTGTCTCGCTGTTGGCCACGAGCTCTGCGGACGAT 1299
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QY 1386 GCTGGTCTCCGTGGGAGAGTGACCCAGCTGCTCCGTGAGCTGTGGCTCTGGGACCCAG 1445
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QY 1360 CAGCGCGCCGCTCTCTCGATAGCGCTCAACAACCGATGTGAGGGCTCTCTCGGTCAGAC 1419
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QY 1505 ACGGCTTGTGAGTGTGACAGCTGTGACACCCGATCCGCGAGCGCGCTCGAGCCA 1564
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QY 1420 ACGACCTGCCACATTCAGGAGTGTGACAGAGATTTAAACAGGATGGTGTGGAGCCA 1479
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QY 1565 CTGCTACCTTGTGTTCTCATCTCTGACCTGTGGAGTTGGCAATATCACACGATCCG 1624
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QY 1480 CTGCTCCCGTGGTCACTTCTTCTGTGACATGTGGTGTGATGATGATCACAAGGATCCG 1539
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QY 1599 GACCAAGCCCTGCAAGAAAGACGCTGCCCATCAATGAGGCTGGGGTCTTGTGTCACTCACC 1658
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QY 1745 GTGGTCCGCTGCACTGTCACTGTGCGGTGGGATCCGGGAGCGCACCCGGGTCTGCAA 1804
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QY 1659 ATGGACATCTGTCTGTCACTGTGGAGGAGGGGTACAGAAACGATGCTCTCTGCA 1718
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QY 1805 CAGCCCTGAGGCTCAGTACGAGGAGAGGCTCGGTGGGGGATGTGAGAGAGCTCAGAT 1864
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QY 1719 CAACCCRCACCCCAAGTTTGGAGCAAGGACTGCGTGTGGTGTATTAACAGAAAAACAGAT 1778
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1865 GTGCAACAAGAGGAGCTGCCCGTGGATGGCTGTTTATCCAAACCCCTCTCTCCGGGAGC 1924
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1779 CTGCAACAAGAGGAGCTGTCCAATTTGATGCTGTCTCAATCCCTGCTTGGCGGCGT 1838
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QY 1925 CCAGTGCAGCAGCTTCCCGGATGGTCTCTGCTCATGGGGCTCTCTGCCCTGTGGCTTCTT 1984
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QY 1839 GAAGTGTACTAGCTACCTGTATGCGAGCTGGAATGTGGTCTTGTCCCTCCCTGGTTACAG 1898
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Qy	1985	GGGCAATGGCACCCCATGTGAGGAOCTGGACGAGTGTGCCCTTGGTCCCGCAGCATCTGCTT	2044
Db	1899	TGGAATGGCATCCAGTGCACAGATGTTGATGAGTGCAAAGAAGTGCCGTGATGCTGCTGTT	1958
Qy	2045	CTCCACCAGCAAGGTGCCTGCTGTGTCAACTCAGCCTGGCTTCCAATGCCTGCCCTG	2104
Db	1959	CAACCAATGGAGAGACCGGTGTGAGAAACAGGACCGCCGGCTACAACTGCCCTGCCCTG	2018
Qy	2105	CCGCCCCGATACAGAGGAACACGCGCTGGGTGGCTGGAGAGCAGCAAGACGGA	2164
Db	2019	CCCCCAGCTTCACCGGCTCAGCGCTTGGCCAGGGTGTGGAACATGCCACGGCCAA	2078
Qy	2165	AAAGCAAGTGTGTGAGCCGGAACCCATGCAAGGACAAGACACAACTGCCACAAGCA	2224
Db	2079	CAAAAGGTGTGCAAGCCCCGTAAACCCCTGCACGGATGGACCCAGCTGCACAAAGAA	2138
Qy	2225	CGCGGATGCATCTACTGGGTCACTTTCAGCGACCCCATGTACAGTGGCGAGTGCCAGAC	2284
Db	2139	CGCAAGTGCAACTACTTGGGCACCTATAGCGACCCCATGTACCGCTGCGAGTCAAAGCC	2198
Qy	2285	AGGCTACGGGGGACGGGCTCATCTGGGGGAGGACTCGGACCTGGACGGCTGGCCCCAA	2344
Db	2199	TGGGTACCTGGCAATGGCATCATCTGGGGGAGGACACAGACTGGATGGCTGGCCCCAA	2258
Qy	2345	CCTCAATGTGTTGCGCCACCAACGCCACTTACACTGCATCAAGGATAACTGCCCCCA	2404
Db	2259	TGAGAACCTGGTGTGCGTGCCCAATGCGACTTACCCTGCAAAAGGATAAATGGCCCAA	2318
Qy	2405	TCGTGCCAATTCGGCGCAGGAGACTTTGCANAGGACGGGATTTGGCGATGCTGTGATGA	2464
Db	2319	CCTTCCCACTCAGGCGAGGAGACTATGCAAGGATGGAAATGGTGTGATGCTGTGATGA	2378
Qy	2465	TGACGATGCAATGACGGGTGCACCGATGAGAAGGACAACCTGCCAGCTCCTCTTCAATCC	2524
Db	2379	TGACGATGCAATGATAAATTCAGATGACAGGGACAACCTGTCCATTCATTAACACC	2438
Qy	2525	CCGCCAGGCTGACTATGACAAGGATCAGGTTTGGGACCGCTGTGACAACCTGCCCTTACGT	2584
Db	2439	AGCTCAGTATGACTATGACAGAGATGATGTGGGACCGCTGTGACAACCTGCCCTACAA	2498
Qy	2585	GCACACCTTGGCCAGATCGACACAGACACAAATGGAGAGGGTGACGCTGCTCCGTGGA	2644
Db	2499	CCACAACCCAGATCAGCGACAGACAGACAACAAATGGGAAGGAGACGCTGTGCTGCAGA	2558
Qy	2645	CAATTGATGGGACGATGCTTCAATGAACGAGACAATTTGCCCTACGCTTACAACACTGA	2704
Db	2559	CATTGATGGAGCGGTATCTCAATGAACGGGACNACTGCCAGTACGCTTACAATGTGGA	2618
Qy	2705	CCAGAGGACACGGATGTGTACGGTGTGGGGATCACTGTGACAACCTGCCCTTGGTGCA	2764
Db	2619	CCAGAGACACTGATATGGATGGGTTGGAGATCAGTGTGACAATTTGCCCTTGGNAACA	2678
Qy	2765	CAACCTTGACCAAGCGAGTGGACAATGACCTTGTGGGACCAAGTGTGACAACACGA	2824
Db	2679	CAATCCGGATCAGCTGGACTGTGACTCAGACCGCAATTTGGAGATACCTGTGACAACATCA	2738
Qy	2825	GGATATAGTACGACGGCCACCAACAACACGAGACAATTCGCCCTTACATCTCCAACGC	2884
Db	2739	GGATATTGATGAGATGGCCACCAGACACAAATCTGGACNACTGTCCCTTATGTGCCCAATGC	2798
Qy	2885	CAACAGGCTGACCATGACAGAGAGCGCCAGGGCAGCCCTGTGACCTGTATGATGACAA	2944
Db	2799	CAACCAAGCTGACCATGACAAAGATGGCAAGCACTGTGAGACTGTGCCCAATCCCACCAAGGA	2858
Qy	2945	CGATGGCTCCCCGATGACAGGGACAACCTGCCGGCTGTGTTCAACCCAGCACGAGNGA	3004
Db	2859	CGATGGCAATCTCTGATGACAAAGGACAACCTGTGAGACTGTGCCCAATCCCACCAAGGA	2918
Qy	3005	CTTGGACGGTGTGACAGGGGTGATATTGTAAAGATGATTTTGCACAAATGACAACATCCC	3064
Db	2919	CTCTGACGGGATGTCGAGGTGATGCTGCAAGAGATGATTTTGACCAATGACAGTGTGCC	2978
Qy	3065	AGATATTGATGTGTGCTCTGAAACAATGCCATCAGTGAGACAGACTTCAGGAACCT	3124

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> RESULT 8
> US-09-954-531-140
> Sequence 140, Application US/09954531
> Patent No. US20020165180A1
> GENERAL INFORMATION:
> APPLICANT: Weaver, Zoe
> TITLE OF INVENTION: Process for Identifying Anti-Cancer Therape
> TITLE OF INVENTION: Gene Sets
> FILE REFERENCE: 689290-77
> CURRENT APPLICATION NUMBER: US/09/954,531
> CURRENT FILING DATE: 2002-05-02
> PRIOR APPLICATION NUMBER: US/60/233,133
> PRIOR FILING DATE: 2000-09-18
> PRIOR APPLICATION NUMBER: US/60/234,009
> PRIOR FILING DATE: 2000-09-20
> PRIOR APPLICATION NUMBER: US/60/234,034
> PRIOR FILING DATE: 2000-09-20
> PRIOR APPLICATION NUMBER: US/60/234,509
> PRIOR FILING DATE: 2000-09-22
> PRIOR APPLICATION NUMBER: US/60/234,567
> PRIOR FILING DATE: 2000-09-22
> NUMBER OF SEQ ID NOS: 1392
> SOFTWARE: PatentIn version 3.0
> SEQ ID NO 140
> LENGTH: 2439

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[illegible]

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Db 825 GTGCGACACTGACCTAGACCTGCTCCCGACGAGAAGCTGGCTGCCCGGAGCCG---- 880
QY 2374 CTTACCACTGCATCAAGGATAACTGCCCCCATCTGCCAAATCTGGCGCAGGAAGACTTGG 2433
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QY 2434 ACAAGGAGGGATGGCGATGCTGTGATGATGACGATGACAATGACGCTGTGACCGATG 2493
Db 936 ACCGCGATGGCATGGAGACGCTGGCATCGGATCGCCAGCGGGGAGCGGGTCCCAATG 995
QY 2494 AGAAGGACACTGCCAGCTCTCTCAATCCCGCCAGCTGACTATGACAAGGATGAGG 2553
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QY 2554 TTGGGACCGCTGTGACAACTGCCCTTACGTGCACAAACCTGCCAGATGCACACAGACA 2613
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QY 2674 GAGACAATTTGCTCCCTACGCTTACACACTGACACAGGAGACAGGATGTGAGCGTGG 2733
Db 1176 CCGACAACCTGCCCTAGGTTACCAACTCAGACCAAGAGACAGTGTGCGGATGTATAG 1235
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QY 2794 ACTTTGTTGGGACCACTGTGACAAACAGAGGACATATGATGACGACGCGCCACCAAGCA 2853
Db 1296 ACTTTGTTGGGAGATGCTTGACAGCGATCAAGACAGGATGGAGCGGACATCAGGACT 1355
QY 2854 ACCAGGACAACTGCCCTACATCTCCAAGCCCAACAGCTGACCATGACAGAGCGGC 2913
Db 1356 CTCGGGACAACTGTCCCGGTGCTTACAGTGCACAGTGCACAGGAGGACTCAGACACGATGGCC 1415
QY 2914 AGGGGACCGCTGTGACCTGATGATGACAAAGGATGGCGTCCCGATGACAGGGACAAT 2973
Db 1416 AGGGTGTGCTTGCACGACGACGACGACAAATGACGGATGCTGACAGTCCGGACAAT 1475
QY 2974 GCGCGTGTGTTCAACCCAGCAGGAGGACTTGGAGGATGATGACGCGGCTGATATTT 3033
Db 1476 GCGCGTGTGCTTAACCCCGCCAGGAGGACGCGACAGGACGCGTGGCGCGAGTGT 1535
QY 3034 GTAAAGATGATTTGACATGACACATCCAGATATTTGATGATGTGTCTGAAACA 3093
Db 1536 GCCAGGACACTTTGATGACAGAAAGGTGGTAGAAGATGACGCTGTGTCGGGAGAACG 1595
QY 3094 ATGCCATGATGACAGACTTCAGGAATTCAGATGGTCCCTTGGATCCCAAGGA 3153
Db 1596 CTGAAGTACGCTACCGACTTCAGGGCTTCCACAGCTGCTGGACCCCGAGGGTG 1655
QY 3154 CCACCCAAATGATCCCACTGGGTCAATTCGCCATCAAGGCAAGGAGCTGTTCAGACAG 3213
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QY 3334 AGTCAAGCAGCGCTTCTATGTGTGATGTGGAAGCAGGTGACGACGACCTACTCGGAGG 3393
Db 1836 AGGACAGCTCCAGCTTCTACGTGGTGTGATGTGGAAGCAGATGAGCAACGATATTGGCAGG 1895
QY 3394 ACCAGCCCAAGCGGCGCTATGCTACTCGGCGCTGTCCCTCAAGGTGGTGAACCTCCACA 3453

Db 1896 CGAAACCCCTTCGCTGTGGCCGAGCCTTGGCATCAACTCAAGGCTGTGAAGTCTTCCA 1955
QY 3454 CGGGGACGGCGAGCACTTGAGGAACCGCTGTGGCACACGGGGGAACACGCGGGGCGAG 3513
Db 1956 CAGGCGCGGGGAACAGCTGCGGAACGCTCTGTGCAATACAGGACACAGAGTCCGAG 2015
QY 3514 TCCGAACCTTATGGACGACCCCGAGAACATTTGGCTGGGAAGACTACAGGCTATAGGT 3573
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RESULT 10
US-10-025-380-327/c
; Sequence 327, Application US/10025380
; Publication No. US20020182191A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tonglong
; APPLICANT: Jiang, Yudi
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C14
; CURRENT APPLICATION NUMBER: US/10/025.380
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 1129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 327
; LENGTH: 619
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 137..490, 493
; OTHER INFORMATION: n = A,T,C or G
US-10-025-380-327

Query Match 10.3%; Score 595.6; DB 9; Length 619;
Best Local Similarity 98.7%; Pred. No. 5.6e-132;
Matches 609; Conservative 0; Mismatches 7; Indels 1; Gaps 1;
QY 4190 TTAAGTTGTCACTATTTCTGAATTTAGAGTTGCTCTACAATGACACACAAATCCG-GCTA 4248
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Db 557 AATAAATTAATAACCAAGGTCGAATTTCAATTTGAAGTAAATTTTGTAGTAAGGAGATTA 498

QY	4309	GAAGACACAGGCATAGCAAAATGACAT	AGCTACCGATTAACTAATCGGAACATGTA	4368
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QY	4429	GAGATGCAGTTTCATCAAGAAACAA	ACATCTCTTGCAAAATGGGTGTGACGCG	4488
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QY	4549	CTGCTGCTTGTCGCGTTGTGGCG	TGCGGAGGCTCCTGCCTGAGCTTCCT	4608
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Db	197	TGCTGCTTGAGAGGAACACAGAG	CACAGCAGCGCGGAAAGCGCATCTA	138
QY	4669	CTAGGCTTTGGTAACTCGGACA	AGTTGCTTTTAACTGATGATACATTT	4728
Db	137	NTAGGCTTTGGTAACTCGGACA	AGTTGCTTTTAACTGATGATACATTT	78
QY	4729	GGTTCCAGTTATAAAATATTTT	GTATATTTTAAAGTGACTATAGAA	4788
Db	77	GGTTCCAGTTATAAAATATTTT	GTATATTTTAAAGTGACTATAGAA	18
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RESULT 11

RESOLUTION
US-09-922-217-327/c
: Sequence 327. Application US/09922217

; Sequence 321, Application
 ; Patent No. US2002007
 ; GENERAL INFORMATION:

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; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.

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APPLICANT: LOUES, MICHAEL J.
APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.

APPLICANT: Benson, Darin
APPLICANT: Meagher, Madeline
APPLICANT: Stolk, John A.

APPLICANT: STOIK, JOHN A.
APPLICANT: Wang, Tongtong
APPLICANT: Jiang, Yugu

;
; AFFILIANT: JIANG, YUQU
; AFFILIANT: SMITH, CAROLE LYNN
; AFFILIANT: KING, GORDON E.

APPLICANT: KING, GORDON E.
APPLICANT: Wang, Aijun
APPLICANT: Clapper, Jonathan D.

APPLICANT: Clapper, Jonathan D.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE

; TITLE OF INVENTION: OF COLON CANCER AND
 ; FILE REFERENCE: 210121.471C13
 ; CURRENT APPLICATION NUMBER: US/09/922,217

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; CURRENT FILING DATE: 2001
; CURRENT APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 1124

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; NUMBER OF SE
; SOFTWARE: Fa
; SEQ ID NO 327

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; SEQ ID NO: 31
; LENGTH: 61
; TYPE: DNA
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; LIFE: DNM
; ORGANISM
; FEATURE:

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;
; NAME/KEY: misc_feature
; LOCATION: 137, 490, 493

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US-09-922-217-327

Best Local Similarity 98.7%; Pred. No. 5.6e-132;
Matches 609; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

RESULT 12

RESULT 12
US-09-8333-263-327/c

US-09-633-203-327/C
; Sequence 327, Application US/09833263
; Patent No. US20020110547A1

; PATENT NO. US2002011
; GENERAL INFORMATION:
; GENERAL INFORMATION:

; GENERAL INFORMATION:
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Clapper, Jonathan D.

; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Stolk, John A.
; APPLICANT: Meagher, Madeleine J.

;; TITLE OF INVENTION: COMPOUNDS
;; TITLE OF INVENTION: DIAGNOSIS

; TITLE OF INVENTION: DIAGNOSIS OF COLEON
 ; FILE REFERENCE: 210121.471C12
 ; CURRENT APPLICATION NUMBER: US/09/833,263

; CURRENT AFFILIATION NUMBER: 05/03/055740
 ; CURRENT FILING DATE: 2001-04-10
 ; NUMBER OF SEQ ID NOS: 1093

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; NUMBER OF SE
; SOFTWARE: FA
; SEQ ID NO 327

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; SEQ ID NO 327
; LENGTH: 619
; TYPE: DNA

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; FILE: DNA
; ORGANISM: Homo sapien
; FEATURE:

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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(619)

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Query Match 10.3%; Score 595.6; DB 10; Length 619;
 Best Local Similarity 98.7%; Pred. No. 5.6e-132;
 Matches 609; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 4190 TTAAGTTGTCACATTTTGAATTAGAGTTGCTCTACAAATGACACACAAATCCC-GCTA 4248
 Db 617 TAAAGTTGTCACATTTTGAATTAGAGTTGCTCTACAAATGACACACAAATCCC-GCTA 558
 QY 4249 AATAAATTAACAAGGTCATTTCAAAATTTGAAGTAATGTTTAAAGGAGAGATTA 4308
 Db 557 AATAAATTAACAAGGTCATTTCAAAATTTGAAGTAATGTTTAAAGGAGAGATTA 498
 QY 4309 GAAGACACAGGATAGCAAAATGACATAAGCTACCGATTAACTAATCGGAACATGTAAAA 4368
 Db 497 GAAGNCTNAGGATAGCAAAATGACATAAGCTACCGATTAACTAATCGGAACATGTAAAA 438
 QY 4369 CAGTTACAAAATAAAGCAACTCTCTCTGTCCTTACAAATGAAGCCCTCATGTCCAGTA 4428
 Db 437 CAGTTACAAAATAAAGCAACTCTCTCTGTCCTTACAAATGAAGCCCTCATGTCCAGTA 378
 QY 4429 GAGATCAGTTTATCAAAAGAACAAACATCTTGGCAATGGGTGTGACGCGGTTCAGAT 4488
 Db 377 GAGATCAGTTTATCAAAAGAACAAACATCTTGGCAATGGGTGTGACGCGGTTCAGAT 318
 QY 4489 GTGGATTGGCAAAACCTCATTTAAGTAAAGGTTAGCAGACAAAGTGGCGGTGCTTTAG 4548
 Db 317 GTGGATTGGCAAAACCTCATTTAAGTAAAGGTTAGTACAGCAAGTGGCGGTGCTTTAG 258
 QY 4549 GTGCTGTTGTGCGGTGTGGCGTGGGGAGGCTCTGCTGCTGAGCTTCTTCCCGAGCTT 4608
 Db 257 GTGCTGTTGTGCGGTGTGGCGTGGGGAGGCTCTGCTGCTGAGCTTCTTCCCGAGCTT 198
 QY 4609 TGTGCTGTGAGGAGAACACAGACAGCAGCGGCGGAAAAAGGCGCATCTAACGCGTAT 4668
 Db 197 TGTGCTGTGAGGAGAACACAGACAGCAGCGGCGGAAAAAGGCGCATCTAACGCGTAT 138
 QY 4669 CTAGGCTTTGGTAACGCGGACAAGTTGCTTTTACCTGATTGATGATACATTTCAATTA 4728
 Db 137 CTAGGCTTTGGTAACGCGGACAAGTTGCTTTTACCTGATTGATGATACATTTCAATTA 78
 QY 4729 GTTCCAGTTAATAATTTTCTTAATATTATTAAGTACATATAGATGCAACTCCATT 4788
 Db 77 GTTCCAGTTAATAATTTTCTTAATATTATTAAGTACATATAGATGCAACTCCATT 18
 QY 4789 TACCAGTAACTTATTTT 4805
 Db 17 TACCAGTAACTTATTTT 1

RESULT 13
 US-09-815-343-1448/c
 ; Sequence 1448, Application US/09815343
 ; Patent No. US2001005596A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Meagher, Madeleine
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: King, Gordon E.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
 ; FILE REFERENCE: 210121.504
 ; CURRENT APPLICATION NUMBER: US/09/815,343
 ; CURRENT FILING DATE: 2001-03-22
 ; NUMBER OF SEQ ID NOS: 1556
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1448
 ; LENGTH: 637
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; LOCATION: (1)...(637)
 ; OTHER INFORMATION: n = A,T,C or G

US-09-815-343-1448
 Query Match 9.3%; Score 540.2; DB 10; Length 637;
 Best Local Similarity 94.9%; Pred. No. 8.6e-119;
 Matches 595; Conservative 0; Mismatches 28; Indels 4; Gaps 4;

QY 4182 TTGGTGTCTTAAAGTTGTCACATTTTGAATTTAGAGTTGCTCTACAAATGACACACAAAT 4241
 Db 626 TTGGTGTCTTAAAGTTGTCACATTTTGAATTTAGAGTTGCTCTACAAATGACACACAAAT 568
 QY 4242 CCGCTAATAATTAATAACAAGGTCACAA-TTCAAAATTTGAAGTAATGCTTTAGT-AAG 4299
 Db 567 TCCNGTTAANAATTTATACCAAGGTCATTTTNAATTTGAAGTAATGCTTTAGTAAAG 508
 QY 4300 GAGATTTAGAAAGACACAGGATAGCAAAATGAC-ATAAGCTTACCAATTAACCTAATTCGA 4358
 Db 507 GAGATTTAGAAAGACACAGGATAGCAAAATGACAAATGACAAATGACCTTACCTAATTCGA 448
 QY 4359 ACATGTAACAGTTTACAAAAATAAACGAACCTCTCTCTGCTTGTCTTACAAATGAAGCCCTC 4418
 Db 447 ACATGTAACAGTTTACAAAAATAAACGAACCTCTCTCTGCTTGTCTTACAAATGAAGCCCTC 388
 QY 4419 ATGTGCTAGATGAGATGCAAGTTTCATCAAGAACAAACATCTCTTGCATTAAGGCTGACGC 4478
 Db 387 ATGTGCTAGATGAGATGCAAGTTTCATCAAGAACAAACATCTCTTGCATTAAGGCTGACGC 328
 QY 4479 GGTTCACAGTTGGATTTGGCAAAACCTCATTTAAGTAAAGGTTAGCAGACCAAGTGC 4538
 Db 327 GGTTCACAGTTGGATTTGGCAAAACCTCATTTAAGTAAAGGTTAGCAGACCAAGTGC 268
 QY 4539 GTGCTTTAGCTGTGCTTGTGCTTGTGGCTGGGGAGGCTCTGCTGAGCTTCTT 4598
 Db 267 GTGCTTTAGCTGTGCTTGTGCTTGTGGCTGGGGAGGCTCTGCTGAGCTTCTT 208
 QY 4599 TCCCGAGCTTTCCTGCTGAGAGAACACAGACAGCAGCAGCAGCGGAAAAAGGCGCATC 4658
 Db 207 TCCCGAGCTTTCCTGCTGAGAGAACACAGACAGCAGCAGCAGCGGAAAAAGGCGCATC 148
 QY 4659 TAACGCTATCTAGGCTTTGGTAACTGGGCAAGTTGCTTTTACCTGATTTGATGATAC 4718
 Db 147 TAACGCTATCTAGGCTTTGGTAACTGGGCAAGTTGCTTTTACCTGATTTGATGATAC 88
 QY 4719 ATTTCATTAAGTTCCAGTTTAAATATTTTGTATTTTAAATTTAAGTACATTAAGAATG 4778
 Db 87 ATTTCATTAAGTTCCAGTTTAAATATTTTGTATTTTAAATTTAAGTACATTAAGAATG 28
 QY 4779 CAACCTCCATTTACCAGTAACTTATTTT 4805
 Db 27 CAACCTCCATTTACCAGTAACTTATTTT 1

RESULT 14
 US-09-920-300A-1233
 ; Sequence 1233, Application US/09920300A
 ; Patent No. US20020136728A1
 ; GENERAL INFORMATION:
 ; APPLICANT: King, Gordon E.
 ; APPLICANT: Meagher, Madeleine Joy
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Secrist, Heather
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; FILE REFERENCE: 210121.547
 ; CURRENT APPLICATION NUMBER: US/09/920,300A
 ; CURRENT FILING DATE: 2001-07-31
 ; NUMBER OF SEQ ID NOS: 1789
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1233
 ; LENGTH: 516
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; OTHER INFORMATION: n = A,T,C or G

Query Match	8.9%; Score 516; DB 10; Length 516;
Best Local Similarity	100.0%; Pred. No. 4.3e-113;
Matches 516; Conservative	0; Mismatches 0; Indels 0; Gaps 0;

QY	4057	AAAAAGAATGACGGTTTACATATAAAATGTAACTATTACTTATTGTATTATTTATGTCTATATGSAG	4116
DB	1	AAAAGAATGACGTTTACATATAAAATGTAACTATTACTTATTGTATTATTTATGTCTATATGSAG	60
QY	4117	TGAAGGGAATGCTGCATAAGCCATTTATGATAAATTAAGCATGAATAATTCGCGAA	4176
DB	61	TGAAGGGAATGCTGCATAAGCCATTTATGATAAATTAAGCATGAATAATTCGCGAA	120
QY	4177	CTACTTTTGGTGCTTAAAGTTGTCACATATCTTGAATTAGAGTTGCTCTACAATGACACA	4236
DB	121	CTACTTTTGGTGCTTAAAGTTGTCACATATCTTGAATTAGAGTTGCTCTACAATGACACA	180
QY	4237	CAATCCCGCTAAATAAATATATAACAAGGTCATTAATCAAATTTGAAGTAATGTTTTAGT	4296
DB	181	CAATCCCGCTAAATAAATATATAACAAGGTCATTAATCAAATTTGAAGTAATGTTTTAGT	240
QY	4297	AAGGAGAGATTAGAAGACACAGGCATAGCAATGACATAAGCTAACGATTAATCTG	4356
DB	241	AAGGAGAGATTAGAAGACACAGGCATAGCAATGACATAAGCTAACGATTAATCTG	300
QY	4357	GACATCTAAACAAGTTACAAAAATAAACAAGCACTCTCCTCTGTGCTTACAAATGAAGCCC	4416
DB	301	GACATCTAAACAAGTTACAAAAATAAACAAGCACTCTCCTCTGTGCTTACAAATGAAGCCC	360
QY	4417	TCATGTCAGTAGAGATGTCAGTTTCATCAAGAACAACATCCTTGGCAATGGGTGTGAC	4476
DB	361	TCATGTCAGTAGAGATGTCAGTTTCATCAAGAACAACATCCTTGGCAATGGGTGTGAC	420
QY	4477	CGGGTCCAGATGTGGATTTGGCAAAACCCTCATTTAAGTAAAGTTAGCAGAGCAAGT	4536
DB	421	CGGGTCCAGATGTGGATTTGGCAAAACCCTCATTTAAGTAAAGTTAGCAGAGCAAGT	480
QY	4537	CGGGTGGCTTTAGCTGCTGCTTGTGCCGCTTGTGGCGT	4572
DB	481	CGGGTGGCTTTAGCTGCTGCTTGTGCCGCTTGTGGCGT	516


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RESULT 15
US-10-033-528-1233
; Sequence 1233, Application US/10033528
; Patent No. US20020131971a1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.547C1
; CURRENT APPLICATION NUMBER: US/10/033,528
; CURRENT FILING DATE: 2001-12-26
; NUMBER OF SEQ ID NOS: 1896
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 1233
; LENGTH: 516
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-528-1233

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	Query Match	8.9%	Score 516;	DB 12;	Length 516;
	Best Local Similarity	100.0%;	Pred. No. 4.3e-113;		
	Matches 516;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	4057	AAAAAGAATCAGCTTTACATATAAAATGTAATCTATTCTATTCTATATCGAG	4116		
Db	1	AAAAAGATCAGCTTTACATATAAATGTAATCTATTCTATTCTATATCGAG	60		
QY	4117	TTCAAGGGAATCTGTGCATAAGCCATTATGCATAAATTAAGCATGAATAATTCGCGAA	4176		

Db	61	TTGAAGGGAATACTGTGCATAAGCCATTATGATAAATTAAGCATGAAAAAATATTGCTGAA	120
Qy	4177	CTACTTTTGGTGCTTAAAGTTGTCATAATTCCTGAATTAGAGTTGCTCTACAANTGACACA	4236
Db	121	CTACTTTTGGTGCTTAAAGTTGTCATAATTCCTGAATTAGAGTTGCTCTACAANTGACACA	180
Qy	4237	CAAAATCCCGCTAAATAAATATATAAACAAGGTCAAATCCAAATTTGCAAGCTAATGTTTTAGT	4296
Db	181	CAAAATCCCGCTAAATAAATATATAAACAAGGTCAAATCCAAATTTGCAAGCTAATGTTTTAGT	240
Qy	4297	AAGGAGAGATTAGAAGACACACAGGCATAGCAATAAGCTACCGATTAACTAATCG	4356
Db	241	AAGGAGAGATTAGAAGACACACAGGCATAGCAATAAGCTACCGATTAACTAATCG	300
Qy	4357	GAACATGTAAACAGTTTACAAAAATAAAGCAACTCTCCTTTGTCTTCAATGAAGGCC	4416
Db	301	GAACATGTAAACAGTTTACAAAAATAAAGCAACTCTCCTTTGTCTTCAATGAAGGCC	360
Qy	4417	TCATGTGCATAGAGATGCAGTTTCATCAAGAACAAACATCCTTGCAAAATGGGTGTGAC	4476
Db	361	TCATGTGCATAGAGATGCAGTTTCATCAAGAACAAACATCCTTGCAAAATGGGTGTGAC	420
Qy	4477	GCGGTTCCAGATGTGGATTGGCAAAACCTCATTTAAGTTAAAGGTTAGCAGAGCAAAAGT	4536
Db	421	GCGGTTCCAGATGTGGATTGGCAAAACCTCATTTAAGTTAAAGGTTAGCAGAGCAAAAGT	480
Qy	4537	GCGGTGCTTTAGCTGCTGCTTGCGCGTTGTGGCGT	4572
Db	481	GCGGTGCTTTAGCTGCTGCTTGCGCGTTGTGGCGT	516

Search completed: December 27, 2002, 04:41:08
Job time : 242 secs

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RESULT 15
US-10-033-528-1233
; Sequence 1233, Application US/10033528
; Patent No. US20020131971A1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.547C1
; CURRENT APPLICATION NUMBER: US/10/033,528
; CURRENT FILING DATE: 2001-12-26
; NUMBER OF SEQ ID NOS: 1896
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1233
; LENGTH: 516
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-528-1233

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[illegible]

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 27, 2002, 00:18:49 ; Search time 4857 Seconds
(without alignments)
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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Listing first 45 summaries

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5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_esthc.*
9: gb_esti.*
10: gb_est2.*
11: gb_hic.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: gb_gss.*
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22: em_gss_fun.*
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27: em_gss_roo.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	791.8	13.7	891	14 BQ925776	BQ925776 AGENCOURT
3	749.2	13.0	937	14 BQ934054	BQ934054 AGENCOURT
4	736	12.7	904	14 BQ940133	BQ940133 AGENCOURT
5	712.2	12.3	794	13 B1758564	B1758564 603023071
6	700.2	12.1	876	9 AU121101	AU121101 AU121101

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8	682.8	11.8	748	12	BG680063	BG680063 602628211
c	675.8	11.7	756	12	BQ008487	BQ008487 UI-H-ED1-
c	663.2	11.5	706	12	BF109743	BF109743 7168c12.x
c	649	11.2	693	10	BE673014	BE673014 7d26h06.x
c	645.2	11.2	660	9	AA149866	AA149866 z147g10.r
13	638.8	11.0	661	13	BM272400	BM272400 1940G09.y
c	635.8	11.0	673	14	BQ002730	BQ002730 UI-H-E11-
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c	629.8	10.9	651	13	BG939270	BG939270 cn31e12.x
c	623.2	10.8	718	9	AI453687	AI453687 tj39a07.x
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c	608.4	10.5	660	14	BM988626	BM988626 UI-H-DH0-
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c	583.8	10.1	615	14	BQ003584	BQ003584 UI-H-E11-
c	580.8	10.0	630	14	BQ017657	BQ017657 UI-H-ED0-
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c	567	9.8	686	9	AI417180	AI417180 tg75g04.x
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c	522	9.0	590	10	AW385593	AW385593 RC3-LT002

ALIGNMENTS

RESULT 1
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LOCUS BQ933301 939 bp mRNA linear EST 21-AUG-2002
DEFINITION AGENCOURT_8744271 Lupski_sciatic_nerve Homo sapiens CDNA clone
IMAGE:6205936 5', mRNA sequence.
ACCESSION BQ933301
VERSION BQ933301.1 GI:22348684
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 939)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution Information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1AM13629 row: j column: 17
High quality sequence stop: 686.
Location/Qualifiers
1. .939

FEATURES
source


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QY 4845 ACAACATCTAATAGTATATATTAATCCCTGTGAAATATGAGG 4886
Db 721 AACAAACATCTAATAGTATATATTAATCCCTGTGAAATATGAGG 762

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LOCUS AGENCOURT_8784556 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:6376342
DEFINITION 5', mRNA sequence.
ACCESSION BO940133
VERSION BO940133.1 GI:22355611
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 904)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM2558 row: f column: 23
High quality sequence stop: 351.
Location/Qualifiers
1. 904
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6376342"
/clone_lib="NIH_MGC_43"
/tissue_type="normal pigmented retinal epithelium"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: eye; Vector: pOTB7; Site: 1; XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. 1"
BASE COUNT 237 a 243 c 249 g 173 t 2 others
ORIGIN
Query Match 12.7% Score 736; DB 14; Length 904;
Best Local Similarity 99.6%; Pred. No. 7.9e-131;
Matches 747; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 2450 CGATGCTGTGATGATGACGATGACATGACGGTGTGACCGATGAGAGGACAACTGCCA 2509
Db 1 CGATGCTGTGATGATGACGATGACATGACGGTGTGACCGATGAGAGGACAACTGCCA 60
QY 2510 GCTCCTCTTCAATCCCGCCAGGCTGACTATGACAAGGATGAGTGGGACCGCTGTGA 2569
Db 61 GCTCCTCTTCAATCCCGCCAGGCTGACTATGACAAGGATGAGTGGGACCGCTGTGA 120

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QY 2570 CAACTGCCCTTACGTGCAACAACCCCTGCCAGATCGACAGACAAACAATGGAGGGTGA 2629
Db 121 CAACTGCCCTTACGTGCAACAACCCCTGCCAGATCGACAGACAAACAATGGAGGGTGA 180
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Db 181 CGCTGCTCCGTGGACATTTGATGGGAGCAGATCTTCAATGAACGAGACAATTTGCCCTA 240
QY 2690 CGTCTACAACTGACACGAGGACACGATGTCACGGTGTGGGGATCACTGTGACAA 2749
Db 241 CGTCTACAACTGACACGAGGACACGATGTCACGGTGTGGGGATCACTGTGACAA 300
QY 2750 CTGCCCCCTGTGTGCACAACCCCTGACACGACCGACCTGGACAATGACCTTGTGGGACCA 2809
Db 301 CTGCCCCCTGTGTGCACAACCCCTGACACGACCGACCTGGACAATGACCTTGTGGGACCA 360
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Db 361 GTGTGACAACAACGAGGACATAGATGACGCGCCACCAACAGACCACTGACCTGCC 420
QY 2870 CTACATCTCCAAACGCGCTGACCATGACAGACGCGCCAGGCGACCGCTGTGA 2929
Db 421 CTACATCTCCAAACGCGCTGACCATGACAGACGCGCCAGGCGACCGCTGTGA 480
QY 2930 CCTGATGATGACAACGATGGCTCCCGGATGACAGGACAACTGCCGGCTTGTGTCAA 2989
Db 481 CCTGATGATGACAACGATGGCTCCCGGATGACAGGACAACTGCCGGCTTGTGTCAA 540
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Db 541 CCCAGACGAGGAGGACTTGGAGCGGTGATGGAGCGGGGTGATATTTGAAGATGATTTGA 600
QY 3050 CAATGACAACATCCAGATATTTGATGATGTCCTGCTGAAACAAATGCCATCAGTACAG 3109
Db 601 CAATGACAACATCCAGATATTTGATGATGTCCTGCTGAAACAAATGCCATCAGTACAG 660
QY 3110 AGACTTCAGGAACTTCCAGATGGTCCCTTGGATCCCAAGGGAGCA-CCCAAAATTTGATC 3168
Db 661 AGACTTCAGGAACTTCCAGATGGTCCCTTGGATCCCAAGGGAGCA-CCCAAAATTTGATC 720
QY 3169 CCAACTGGGTGATTCGCCATCAAGCAAGG 3198
Db 721 CCAACTGGGTGATTCGCCATCAAGCAAGG 750

RESULT 5
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LOCUS 603023071f1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5193785 5',
DEFINITION mRNA sequence.
ACCESSION BO940133
VERSION BO940133.1 GI:15750142
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 794)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM11484 row: m column: 18
High quality sequence start: 29

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FEATURES
source
High quality sequence stop: 783.
Location/Qualifiers
1. .794
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5193785"
/lab_host="NIH_MGC_114"
/lab_host="DH10B"
/Note="Organ: Brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH_MGC Library."
BASE COUNT 162 a 247 c 238 g 147 t
ORIGIN
Query Match 12.3%; Score 712.2; DB 13; Length 794;
Best Local Similarity 97.9%; Pred. No. 2.9e-126;
Matches 753; Conservative 0; Mismatches 13; Indels 3; Gaps 3;
QY 106 CCGGAGCATCTGCACCTGCGGCGGCTCTCGCTCCAGCAGAGCTGGCCCTTCTGA 165
DB 27 CCGGAGCATCTGCACCTGCGGCGGCTCTCGCTCCAGCAGAGCTGGCCCTTCTGA 86
QY 166 CTCGGTCCGGAACACTGAAACCACTATCATCTGCTCTTTTGGCAACACGAGCTCAG 225
DB 87 CTCGGTCCGGAACACTGAAACCACTATCATCTGCTCTTTTGGCAACACGAGCTCAG 146
QY 226 CTCGAGGAGGAGGATGGTCTGAGGCTGCTCTGCTGCTCTGCTGCTGCTGCTGCTG 285
DB 147 CTCGAGGAGGAGGATGGTCTGAGGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 206
QY 286 CGCAAGCTGCTGACAGCAACAGACAGCTTCTGACCTTTTCAGTATCAGCACATCA 345
DB 207 CGCAAGCTGCTGACAGCAACAGACAGCTTCTGACCTTTTCAGTATCAGCACATCA 266
QY 346 ACCCAAGACCATTTGGGCGCCAAAGCAGTTCCGCGGCGCCGAGCCCGGCTTACC 405
DB 267 ACCCAAGACCATTTGGGCGCCAAAGCAGTTCCGCGGCGCCGAGCCCGGCTTACC 326
QY 406 GCTTGTGCGGTTTGCATACATCCACCGGTGAACGAGATGACCTCAGCAAGATCACC 465
DB 327 GCTTGTGCGGTTTGCATACATCCACCGGTGAACGAGATGACCTCAGCAAGATCACC 386
QY 466 AGATCATGCGGCAAGAGGCGCTTCTCTCAGCGGCCAGCTCAAGCAGGACGCGAAGT 525
DB 387 AGATCATGCGGCAAGAGGCGCTTCTCTCAGCGGCCAGCTCAAGCAGGACGCGAAGT 446
QY 526 CCAGGGGACGCTGTTGGCTCTGGAGGCGCCCGTCTCTCCAGAGGACGTTCCAGATCG 585
DB 447 CCA-GGGCAGCGCTGTTGGCTCTGGAGGCGCCCGTCTCTCCAGAGGACGTTCCAGATCG 505
QY 586 TCTCCAGGCGCCCGCGGACAGCTGATCTCAGCTTACTGATTCAGGACGCGGCGATG 645
DB 506 TCTCCAGGCGCCCGCGGACAGCTGATCTCAGCTTACTGATTCAGGACGCGGCGATG 565
QY 646 TGGTCTCCCTGGAGGAGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 705
DB 566 TGGTCTCCCTGGAGGAGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 625
QY 706 TGGCTGGCAGACCTACAGCTTGCAGCTGGGCTGCGGCTGCGGCTCATAGGACGCTGCTCTGG 765
DB 626 TGGCTGGCAGACCTACAGCTTGCAGCTGGGCTGCGGCTCATAGGACGCTTGCCTCTGG 685
QY 766 ACAGAGCCCTTCTAGAGGACCTGCA-GGGGAAAGAGCGCGGATGTACGTGGCCAAAGGC 824
DB 686 ACAGAGCCCTTCTAGAGGACCTGCAAGAGGCGGACAAAGAGCGCGGATGTACGTGGCCAAAGGC 745
QY 825 TCTGCC-AGAGAGAGTCACTTCAGGGGTTGCTTTCAGACAGCTCCACCTA 872
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Db 746 TCTGCCAAGAGAGAGTCACTTCAGGGGTTAGCTTCAGAACGTCACCTA 794
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RESULT 6
LOCUS AUI21101 876 bp mRNA linear EST 01-AUG-2002
DEFINITION AUI21101 HEMBB1 Homo sapiens cDNA clone HEMBB1002084 5', mRNA
sequence.
ACCESSION AUI21101
VERSION AUI21101.1 GI:10936336
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 876)
AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
Isogai,T.
TITLE HRI human cDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix
Research Institute; cDNA library construction; Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
LOCATION/Qualifiers
source
1. .876
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HEMBB1002084"
/tissue_type="whole embryo, mainly body"
/dev_stage="embryo, 10 weeks"
/Note="vector: pME18SFL3"
BASE COUNT 230 a 207 c 238 g 197 t 4 others
ORIGIN
Query Match 12.1%; Score 700.2; DB 9; Length 876;
Best Local Similarity 99.6%; Pred. No. 5.8e-124;
Matches 702; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3048 GACAATGACACATCCCAGATATTGATGATGTGTCTCTGAAACAAATGCCATCAGTGAG 3107
DB 1 GACAATGACACATCCCAGATATTGATGATGTGTCTCTGAAACAAATGCCATCAGTGAG 60
QY 3108 ACAGACTTCAGAACTTCCAGATGGTCCCTTGGATCCCAAGGGACCAACCAATTGAT 3167
DB 61 ACAGACTTCAGAACTTCCAGATGGTCCCTTGGATCCCAAGGGACCAACCAATTGAT 120
QY 3168 CCCAACTGGGTCAITTCGCCATCAAGGCAAGGAGCTGGTTCCAGACAGCCAACTCGGACCCC 3227
DB 121 CCCAACTGGGTCAITTCGCCATCAAGGCAAGGAGCTGGTTCCAGACAGCCAACTCGGACCCC 180
QY 3228 GGCATCGCTGTAGGTTTTCAGCAGATTTGGGTCTGTGGACTTCAGTGGGCACATTCACGTA 3287
DB 181 GGCATCGCTGTAGGTTTTCAGCAGATTTGGGTCTGTGGACTTCAGTGGGCACATTCACGTA 240
QY 3288 AACACTGACCGGGACGAGCTATGCTGCTTCTGCTTGTGTACCTCAGCAGGCGCG 3347
DB 241 AACACTGACCGGGACGAGCTATGCTGCTTCTGCTTGTGTACCTCAGCAGGCGCG 300
QY 3348 TTCTATGTGGTGATGTGAAGCAGGTGACGAGAGCTACTGGGAGGACGAGCCACGCGG 3407
DB 301 TTCTATGTGGTGATGTGAAGCAGGTGACGAGAGCTACTGGGAGGACGAGCCACGCGG 360
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QY 3408 GCCTATGGCTACTCGGGCGTGTCCCTCAAGGTGGTGAAGTCCACACACGGGGACGGCGAG 3467
Db 361 GCGCTATGGCTACTCGGGCGTGTCCCTCAAGGTGGTGAAGTCCACACACGGGGACGGCGAG 420
QY 3468 CACCTGAGGAACCGCTGTGGGCACACGCGGGGACACCGCGGGCAGGTGCGAACCTTATGG 3527
Db 421 CACCTGAGGAACCGCTGTGGGCACACGCGGGGACACCGCGGGCAGGTGCGAACCTTATGG 480
QY 3528 CACGACCCCGAGGAACATTTGCTGGAAGGACTACACGGGCTATAGTGGCCACTGACTCAC 3587
Db 481 CACGACCCCGAGGAACATTTGCTGGAAGGACTACACGGGCTATAGTGGCCACTGACTCAC 540
QY 3588 AGGCCACAGACCGGTACATCAGAGCTTTAGTGCATGAAAGAAACACAGTCAATGCGCAG 3647
Db 541 AGGCCACAGACTGGCTACATCAGAGCTTTAGTGCATGAAAGAAACACAGTCAATGCGCAG 600
QY 3648 TCAGGACCTATCTATGACCAACCTACGCTGCGGGCGGCTGGGCTATTTGCTCTTCT 3707
Db 601 TCAGGACCTATCTATGACCAACCTACGCTGCGGGCGGCTGGGCTATTTGCTCTTCT 660
QY 3708 CAAGAAATGGTCTATTTCTCAGACCTCAAGTACGAATGCAGAGAT 3752
Db 661 CAAGAAATGGTCTATTTCTCAGACCTCAAGTACGAATGCAGAGAT 705

RESULT 7
BM718851
LOCUS
DEFINITION
  UI-E-E01-a-jc-j-23-0-UI.r1 UI-E-E01 Homo sapiens cDNA clone
  UI-E-E01-a-jc-j-23-0-UI 5', mRNA sequence.
ACCESSION
  BM718851
VERSION
  BM718851.1 GI:19037242
KEYWORDS
  EST.
SOURCE
  human.
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
  1 (bases 1 to 721)
  Bonaldo,M.F., Lennon,G. and Soares,M.B.
  Normalization and subtraction: two approaches to facilitate gene
  discovery
  Genome Res. 6 (9), 791-806 (1996)
  9704477
  Contact: Soares, MB
  Program for Rat Gene Discovery and Mapping
  University of Iowa
  451 Eckstein Medical Research Building Iowa City, IA 52242, USA
  Tel: 319 335 8250
  Fax: 319 335 9565
  Email: msoares@blue.weeg.uiowa.edu
  Tissue Procurement: Dr. Gregg Hageman
  cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
  cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
  DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
  Clone Distribution: Researchers may obtain clones from Research
  Genetics (www.resgen.com).
  Seq primer: M13 Reverse.
  Location/Qualifiers
    1..721
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      /db_xref="taxon:9606"
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      /clone_lib="UI-E-E01"
      /tissue_type="fetal eye"
      /dev_stage="fetal"
      /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
      /note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a
      modified polylinker; Site_1: EcoR I; Site_2: Not I;
      UI-E-E01 is a normalized cDNA library containing the
      following tissue(s): fetal eye. The library was
      constructed according to Bonaldo, Lennon and Soares,
      Genome Research, 6:791-806, 1996. First strand cDNA
      synthesis was primed with an oligo-dT primer containing a

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Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT73-pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
GCGCTATACC. This library was created for the program, Gene
Discovery in the Visual System, supported by National Eye
Institute (NEI).
BASE COUNT      238 a      123 c      156 g      204 t
ORIGIN

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Query Match      12.0%; Score 694.8; DB 14; Length 721;
Best Local Similarity 99.4%; Pred. No. 6.4e-123;
Matches 718; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 3921 GCCTTTCAGAGGATAATATCAATGAACTCAGAGATGAACATCTAACCC-ACATAGAGAA 3979
Db 1 GCCTTTCAGAGGATAATATCAATGAACTCAGAGATGAACATCTAACCCACTAGAGAA 60
QY 3980 ACCAGTTGGTGATATGAGACTTTTATGTGGAGTGAATAATGGGCATGCCATTACATTG 4039
Db 61 ACCAGTTGGTGATATGAGACTTTTATGTGGAGTGAATAATGGGCATGCCATTACATTG 120
QY 4040 CTTTTCCTGTTGTTTAAAGAAATGACGTTTACATATAAAATGTAATTTACTTTATGTA 4099
Db 121 CTTTTCCTGTTGTTTAAAGAAATGACGTTTACATATAAAATGTAATTTACTTTATGTA 180
QY 4100 TTTATGCTATATGAGTGTGAAGCAATACGTTGATAGCCATTATGATAAATTAAGCA 4159
Db 181 TTTATGCTATATGAGTGTGAAGCAATACGTTGATAGCCATTATGATAAATTAAGCA 240
QY 4160 TGAATAATTTGCTGAACACTCTTTTGGTGTCTTAAAGTGTCTACTATTTCTTGAATTAGAGT 4219
Db 241 TGAATAATTTGCTGAACACTCTTTTGGTGTCTTAAAGTGTCTACTATTTCTTGAATTAGAGT 300
QY 4220 TGCTCTACATGACACACAAATCCCGCTTAAATTAATAACAGAGGTCAATTCAAATT 4279
Db 301 TGCTCTACATGACACACAAATCCCGCTTAAATTAATAACAGAGGTCAATTCAAATT 360
QY 4280 TGAAGTAAATGTTTAAAGGAGAGATTAGAGACACAGGATAGCAATGACATAGC 4339
Db 361 TGAAGTAAATGTTTAAAGGAGAGATTAGAGACACAGGATAGCAATGACATAGC 420
QY 4340 TACGATTAACTAACTCGGAACATGTAAACACAGTTTACAAAAATFAAACAGACTCTCTCTTG 4399
Db 421 TACGATTAACTAACTCGGAACATGTAAACACAGTTTACAAAAATFAAACAGACTCTCTCTTG 480
QY 4400 TCCTACAAATGAAGCCCTCATGTGCGAGTAGAGATGCGATTTTCATCAAAAGACAAACATCC 4459
Db 481 TCCTACAAATGAAGCCCTCATGTGCGAGTAGAGATGCGATTTTCATCAAAAGACAAACATCC 540
QY 4460 TTGCAATGGGTGTGACCGGTTCAGATGCGATTTGCGAAACCTCATTTAAGTAAAA 4519
Db 541 TTGCAATGGGTGTGACCGGTTCAGATGCGATTTGCGAAACCTCATTTAAGTAAAA 600
QY 4520 GGTTAGCAGACAAAGTCCGCTGCTTTAGCTGCTGTGCGGTGCGGTGCGGGAG 4579
Db 601 GGTTAGCAGACAAAGTCCGCTGCTTTAGCTGCTGTGCGGTGCGGTGCGGGAG 660
QY 4580 GCTCTGCTGAGCTTCCCTCCAGCTTTGCTGCGTGAAGGAACACAGAGCAGCAGC 4639
Db 661 GCTCTGCTGAGCTTCCCTCCAGCTTTGCTGCGTGAAGGAACACAGAGCAGCAGC 719
QY 4640 AG 4641
Db 720 AG 721

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RESULT 8
AI346330/c
LOCUS
DEFINITION qp50808.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926422 3'
973 bp mRNA linear EST 02-FEB-1999

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similar to gb:L12350 THROMBOSPONDIN 2 PRECURSOR (HUMAN);, mRNA
sequence.
ACCESSION AI346330
VERSION AI346330.1 GI:4083536
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 793)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1324 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 456.
Location/Qualifiers
1. 793
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1926422"
/clone_lib="NCI-CCAP_C08"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
colon adenocarcinoma, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT73
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo."
2 others
BASE COUNT 198 a 191 c 186 g 216 t
ORIGIN
Query Match 11.8%; Score 683.4; DB 9; Length 793;
Best Local Similarity 95.88; Pred. No. 9.7e-121;
Matches 744; Conservative 0; Mismatches 28; Indels 5; Gaps 4;

QY 3392 GGACGAGCCCGGCGCTATGCTACTCGGCGTGTCCCTCAAGGTGTGAACCTCCAC 3451
DB 773 GGAGAACGCCACCGGCTTAATGGTACTCGGNGTGT-CCTCAAGGTGTGA--CTCAC 717

QY 3452 CACGGGACGGGCGGACGACCTGAGGACGCGCTGTGGACACGGGGGACCGCGGGGCA 3511
DB 716 CACGGGACGGGCGGACGACCTAGGAGAACGCGTGTGGTGGACACCGGGGACCGCGGGGCA 657

QY 3512 GGTGCGAACCTTATGGCAGCAGCCCGGAGCAATTTGGCTTGGAGGACTACACGGCTATAG 3571
DB 656 GGTGCGAA-CTTATGGCAGCAGCCCGGAGCAATTTGGCTTGGAGGACTACACGGCTATAG 598

QY 3572 GTGGCAGCTGACTCAGAGGCCCGGAGCGGCTACATCAGAGTCTTAGTGCATGAAGGAAA 3631
DB 597 GTGGCAGCTGACTCAGAGGCCCGGAGCGGCTACATCAGAGTCTTAGTGCATGAAGGAAA 538

QY 3632 ACAGGTATGGCAGACTCAGGACCTATCTATGACCAACCTACCTGGCGGGCGGCTGGG 3691
DB 537 ACAGGTATGGCAGACTCAGGACCTATCTATGACCAACCTACCTGGCGGGCGGCTGGG 478

QY 3692 TCTATTTGCTCTCTCAAGAAATGGTCTATTTCTCAGACCTCAAGTACGAGTACGAGA 3751
DB 477 TCTATTTGCTCTCTCAAGAAATGGTCTATTTCTCAGACCTCAAGTACGAGTACGAGA 418

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QY 3752 TATTTAAACAAGATTGCTGTCATTTCCGGCAATG-CCTGTGTCATGCCATGGTCCCTAGA 3810
DB 417 TATTTAAACAAGATTGCTGTCATTTCCGGCAATGCGCCCTGTGCATGCCATGGTCCCTAGA 358
QY 3811 CACCTCAGTTTCATTTGCTGCTTGGGCTTCTCTCTAGCAGACCTCCTGTGCTCCCTTGA 3870
DB 357 CACCTCAGTTTCATTTGCTGCTTGGGCTTCTCTCTAGCAGACCTCCTGTGCTCCCTTGA 298
QY 3871 CTTTAACCTCTGATGTTCTTCCACCTCTCCGAGCAACCCCAACCCCAAGTGCCTTCAGAG 3930
DB 297 CTTTAACCTCTGATGTTCTTCCACCTCTCCGAGCAACCCCAACCCCAAGTGCCTTCAGAG 238
QY 3931 GATAAATATCAATGGAACCTCAGAGATGAACATCTAAACCCACTAGAGAAACAGTTTGGT 3990
DB 237 GATAAATATCAATGGAACCCAGAGATGAACATCTAAACCCACTAGAGAAACAGTTTGGT 178
QY 3991 GATATATGAGACTTATGTGGAGTGAAATTTGGGATGCCATTCATATGCTTTTCTTGT 4050
DB 177 GATATATGAGACTTATGTGGAGTGAAATTTGGGATGCCATTCATATGCTTTTCTTGT 118
QY 4051 TTGTTTAAAGAAATGAGCTTTACATATATAAATGTAATTAATTTATTTATTTATGTTAT 4110
DB 117 TTGTTTAAAGAAATGAGCTTTACATATATAAATGTAATTAATTTATTTATTTATGTTAT 58
QY 4111 ATGGAGTTGAAGGGAATCTGTGATGATGATGATGATGATGATGATGATGATGATGAT 4167
DB 57 ATGGAGTTGAAGGGAATCTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1

RESULT 9
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LOCUS 6026282211F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4753130 5',
DEFINITION mRNA sequence.
ACCESSION BG680063
VERSION BG680063.1 GI:13911460
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 748)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10612 row: e column: 03
High quality sequence stop: 747.
Location/Qualifiers
1. 748
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/db_xref="taxon:9606"
/clone="IMAGE:4753130"
/clone_lib="NCI_CGAP_Skn4"
/tissue_type="squamous cell carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site: 1; NotI;
Site: 2; SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 216 a 113 c 131 g 288 t
ORIGIN
Query Match 11.8%; Score 682.8; DB 12; Length 748;

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Best Local Similarity: 97.3%; Pred. No. 1.3e-120; Mismatches 0; Indels 8; Gaps 3;

QY 4719 ATTTCATTAAAGGTTCCAGTATATAATATTTTGTATATTTTAAAGTACGATAGAAATG 4778
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Db 1 ATTTCATTAAAGTTCAGTATATAATATTTTGTACTATTTTAAATTCACATAGAAATG 60

QY 4779 CAATCCATTTACCAGTACTATTTTAAATATGCTAGTACACATATGTAGTATAAT 4838
|||||
Db 61 CAATCCATTTACCAGTACTATTTTAAATATGCTAGTACACATATGTAGTATAAT 120

QY 4839 TCTAGAAACAAACATCTAATAAGTATATAATCTGTGAAATATGAGCTTATATATTT 4898
|||||
Db 121 TCTAGAAACAAACATCTAATAAGTATATAATCTGTGAAATATGAGCTTATATATTT 180

QY 4899 AGGTTGTCCAGTGAAGCATGCTAGAAGCTGTAAACAGATACATAGAGATAATATGAGGAG 4958
|||||
Db 181 AGGTTGTCCAGTGAAGCATGCTAGAAGCTGTAAACATATACATAGAGATAATGAGGAG 240

QY 4959 TTTATGATGGAACCTTAATATATATATGTTGCCAGGATTTTGTAGTCAATATTTGTACTG 5018
|||||
Db 241 TTTATGATGGAACCTTAATATATATATGTTGCCAGGATTTTGTAGTCAATATTTGTACTG 300

QY 5019 TTATCTATCTGCTATATGGAATCTTTTAAATCAAAAGCTGAAACGAATCAGCATTT 5078
|||||
Db 301 TTATCTATCTGCTATATGGAATCTTTTAAATCAAAAGCTGAAACGAATCAGCATTT 360

QY 5079 AGTCTTGCCAGGCACACCAATTAATCAGTCATGTGTATATGCAAAAGTTTGTGTTTGT 5138
|||||
Db 361 AGTCTTGCCAGGCACACCAATTAATCAGTCATGTGTATATGCAAAAGTTTGTGTTTGT 420

QY 5139 TTTGTTTTTTTT-----GTTGTTGGTTTTTTTGGTTTAAAGTTGATGATCTTCGCGAG 5193
|||||
Db 421 TTTGTTTTTTTTTTGTTGTTGTTGTTTGTGTTTAAAGTTGATGATCTTCGCGAG 480

QY 5194 GAAATAGTCATCTATCCACTCCACATAGGGGTTTGTAGTAAGAGAGTCTGCTGCTGA 5253
|||||
Db 481 GAAATAGTCATCTATCCACTCCACATAGGGGTTTGTAGTAAGAGAGTCTGCTGCTGA 540

QY 5254 TGATGATAGGGGGCAATCTTTTCCCTTTCTGTTTAAATGATCATCATCTTCTATGCC 5313
|||||
Db 541 TGATGATAGGGGGCAATCTTTTCCCTTTCTGTTTAAATGATCATCATCTTCTATGCC 600

QY 5314 AAACAGGAACGATCATCACTTATGCTTAATGATACATTCATTCATTTGATATAATAT 5373
|||||
Db 601 AAACAGGAACGATCATCACTTATGCTTAATGATACATTCATTTGATATAATAT 660

QY 5374 TTTGTTGTTTCTTTGAGGTTGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5431
|||||
Db 661 TTTGTTGTTTCTTTGAGGTTGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 720

QY 5432 GCGTGTGGAGCTG-TATTCCCGAGACAA 5458
|||||
Db 721 GCGTGTGGAGCTGTTATTCCCGAGACAA 748

RESULT 10
BQ008487/c
LOCUS
DEFINITION UI-H-ED1-ayk-b-03-0-UI-s1 NCI_CGAP_ED1 Homo sapiens CDNA clone
IMAGE:5839778 3', mRNA sequence.

ACCESSION BQ008487
VERSION BQ008487.1 GI:19733388
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 756)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
The following repetitive elements were found in this cDNA
sequence: 637-685, >(CAAA)n#simple_repeat
Seq primer: M13 FORWARD
POLYA-Yes.

FEATURES

Location/Qualifiers
source
1..756

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/lab_host="DH10B (Life Technologies)"
/note="Organ: Left Pubic Bone; Vector: pT7T3-Pac
(Pharmacia) with a modified polylinker; Site_1: EcoR I;
Site_2: Not I; NCI_CGAP_ED1 is a normalized cDNA library
containing the following tissue(s): Chondrosarcoma cell
line C8S. The library was constructed according to Bonaldo
, Lennon and Soares, Genome Research, 6:791-806, 1996.
First strand cDNA synthesis was primed with an oligo-dT
primer containing a Not I site. Double stranded cDNA was
ligated to an EcoR I adaptor, digested with Not I, and
cloned directionally into pT7T3-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is GCTCAAGGCT.
TAG_L1IB-UI-H-ED1
TAG_ISSUE=chondrosarcoma
TAG_SEQ=CGTCAAGGCT"

BASE COUNT 280 a 145 c 117 g 213 t 1 others
ORIGIN

Query Match 11.7%; Score 675.8; DB 14; Length 756;
Best Local Similarity 98.4%; Pred. No. 2.8e-119;
Matches 726; Conservative 0; Mismatches 3; Indels 9; Gaps 4;

QY 5056 ACGCTGAAAACGAATCAGCATTTAGTCTTGCCAGGCACACCAATAATCAGTCATGTGTA 5115
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Db 756 ACGCTGAAAACGAATCAGCATTTAGTCTTGCCAGGCACACCAATAATCAGTCATGTGTA 697

QY 5116 ATATGCAC-AAAGTTGTTTGTGTTTGTGTTTGTGTTGTTGTTGTTGTTGTTGTTGTT 5170
|||||
Db 696 ATATGCACAAAGTTGTTTGTGTTTGTGTTTGTGTTTGTGTTGTTGTTGTTGTTGTT 637

QY 5171 TAAAGTTGATGATCTTCTGCGAGGAATAGTCACATCCCACTCCACATAGGGGTTTA 5230
|||||
Db 636 TAAAGTTGATGATCTTCTGCGAGGAATAGTCACATCCCACTCCACATAGGGGTTTA 577

QY 5231 GTAGAGAAAGTCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 5290
|||||
Db 576 GTAGAGAAAGTCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 517

QY 5291 AATAGTCATCATCTTCTATGCCAAACAGGAACGATCCATCACTTACTTAAAGTACATA 5350
|||||
Db 516 AATAGTCATCATCTTCTATGCCAAACAGGAACGATCCATCACTTACTTAAAGTACATA 457

QY 5351 CATTCATTTGATAAAATTAATTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTT 5407
|||||
Db 456 CATTCATTTGATAAAATTAATTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTT 397

QY 5408 TTTTGCTGCACATTTTACTTTTTCGCGTGGAGCTGTATTCGCCGAGA-CACACGAAGCGT 5466
|||||
Db 396 TTTTGCTGCACATTTTACTTTTTCGCGTGGAGCTGTATTCGCCGAGACCAACGAAGCGT 337


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QY 5467 TGGGATACCTTCATTAATGTAGCAGCTGCTCAACAGCGTCGAGGCTTTCTGTTCTGTTGTT 5526
Db 336 TGGGATACCTTCATTAATGTAGCAGCTGCTCAACAGCGTCGAGGCTTTCTGTTCTGTTGTT 277
QY 5527 GTGGGGTCAACCGTACAAATGTGTGGGAATGACGATGATGTAATATTTAGAAATGTACCA 5586
Db 276 GTGGGGTCAACCGTACAAATGTGTGGGAATGACGATGATGTAATATTTAGAAATGTACCA 217
QY 5587 TATTTTGTGAAATATTTATGTTTTTCTAAACAAATTTATCGATATAGTTGATGAAACG 5646
Db 216 TATTTTGTGAAATATTTATGTTTTTCTAAACAAATTTATCGATATAGTTGATGAAACG 157
QY 5647 TCATGTGTTTTGCCAAAGACTGTAATATTTATTTATGTTGTCACATGGTCAAAATTTCA 5706
Db 156 TCATGTGTTTTGCCAAAGACTGTAATATTTATTTATGTTGTCACATGGTCAAAATTTCA 97
QY 5707 CCAGTGAACCCCTGCACTTACGTAGAACCTCAATTTTAAAGATTAAACACAGGAATATAA 5766
Db 96 CCAGTGAACCCCTGCACTTACGTAGAACCTCAATTTTAAAGATTAAACACAGGAATATAA 37
QY 5767 TTGTAAAAAGGTTTTCT 5784
Db 36 TTGTAAAAAGGTTTTCT 19

RESULT 11
BF109743/c
LOCUS
DEFINITION
7168c12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
IMAGE:3526654.3' similar to SW:TSPI_BOVIN Q28178 THROMBOSPONDIN 1
; mRNA sequence.
BF109743
BF109743.1 GI:10939433
EST.
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 706)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cyapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Glibco
High quality sequence stop: 470.
Location/Qualifiers
FEATURES
source
1..706
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3526654"
/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
/notes="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from five normalized
libraries were mixed, and ss circles were made in vitro.
Following HAP purification, this DNA was used as tracer in
a subtractive hybridization reaction. The driver was
PCR-amplified cDNAs from pools of 5,000 clones made from
the same 5 libraries. The pools consisted of the following
libraries and clones: Soares NBHSP pool 1:
309384-310919, 323208-325895 Soares NB2HP pool 1:
145032-147335, 147720-148103, 148872-149255, 15002 -
150407, 151176-152327 Soares NB2HF8-9W pool 1:
738280-760583, 772104-774407 Soares NBHPA pool 1:
304776-306311, 320136-322823, 326280-326663 Soares NBHOT
pool 1: 723720-726407, 739080-740999 Subtraction by Bento
Soares and M. Fatima Bonaldo."
208 a 138 c 153 g 206 t 1 others
BASE COUNT
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ORIGIN

Query Match 11.5%; Score 663.2; DB 12; Length 706;
Best Local Similarity 97.2%; Pred. No. 7.3e-117;
Matches 685; Conservative 0; Mismatches 19; Indels 1; Gaps 1;

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QY 3573 TGGCACCCTGACTCACAGGCCCAAGACCGGTACATCAGAGTCTTAGTGCATGAAGGAAA 3632
Db 706 TGGCACCCTGACTCCAGGCCCAAGACCTGGTACCATCAGAGTCTTAGTGCATGAGGGAATC 647
QY 3633 CAGGTCTATGGCAGACTCAGGACCTATCTATGACCAAACTACGCTGGCGCGCGTGGT 3692
Db 646 CAGGTCTATGGCAGACTCAGGACCTAT-TATACCCCAACCTACCGCTGGCGCGCGTGGT 588
QY 3693 CTATTTGCTTCTCTCAAGAAATGGTCTATTTCTCAGACCTCAAGTACGAGAT 3752
Db 587 CTATTTGCTTCTCTCAAGAAATGGTCTATTTCTCAGACCTCAAGTACGAGAT 528
QY 3753 ATTTAAACAAGATTTGCTGCAATTTCCGGCAATGCCCTGTCATGCCATGGTCCCTAGACA 3812
Db 527 ATTTAAACAAGATTTGCTGCAATTTCCGGCAATGCCCTGTCATGCCATGGTCCCTAGACA 468
QY 3813 CCTCAGTTTCTTGTGGCTTCTCTCTCTAGCAGCACTCCTCTGTCCTTGGTACC 3872
Db 467 CCTCAGTTTCTTGTGGCTTCTCTCTCTAGCAGCACTCCTCTGTCCTTGGTACC 408
QY 3873 TTAACCTCTGATGTTTCTTCACTCTCTGCGCAACCCCAACCCCAAGTCCCTTCAGAGGA 3932
Db 407 TTAACCTCTGATGTTTCTTCACTCTCTGCGCAACCCCAACCCCAAGTCCCTTCAGAGGA 348
QY 3933 TAAATATCAATGGAACCTCAGAGATGAACATCTAACCCCTAGAGGAACCAAGTTGGTGA 3992
Db 347 TAAATATCAATGGAACCTCAGAGATGAACATCTAACCCCTAGAGGAACCAAGTTGGTGA 288
QY 3993 TATATGAGACTTTATGTGGAGTGAAATTTGGGCATGCCATTCATTTCTTCTTCTTCTT 4052
Db 287 TATATGAGACTTTATGTGGAGTGAAATTTGGGCATGCCATTCATTTCTTCTTCTTCTT 228
QY 4053 GTTTAAAAAAGAAATGACGTTTACATATAAAATGTAATTAATTAATTAATTAATTAATTA 4112
Db 227 GTTTAAAAAAGAAATGACGTTTACATATAAAATGTAATTAATTAATTAATTAATTAATTA 168
QY 4113 GGAGTTGAAGGGAATGCTGTCATAGCCATTTATGATAAATTAAGCATGAAATATTTGC 4172
Db 167 GGAGTTGAAGGGAATGCTGTCATAGCCATTTATGATAAATTAAGCATGAAATATTTGC 108
QY 4173 TGAACCTACTTTTGTGCTTAAAGTTGTCACATTTCTTGAATAGAGTTGCTCTACAATGA 4232
Db 107 TGAACCTACTTTTGTGCTTAAAGTTGTCACATTTCTTGAATAGAGTTGCTCTACAATGA 48
QY 4233 CACACAAATCCCGCTAAATAAATTTATAACAAAGGTCAATTTCAA 4277
Db 47 CACACAAATCCCGCTAAATAAATTTATAACAAAGGTCAATTTCAA 3
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RESULT 12
BE673014/c
LOCUS
DEFINITION
7426h06.x1 NCI-CGAP Pr28 Homo sapiens cDNA clone IMAGE:3248411 3'
similar to gb:L12350 THROMBOSPONDIN 2 PRECURSOR (HUMAN);, mRNA
sequence.
ACCESSION
VERSION BE673014
KEYWORDS BE673014.1 GI:10033555
SOURCE EST.
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 693)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)

RESULT 15
BQ002730/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BQ002730 673 bp mRNA linear EST 26-MAR-2002
UI-H-E11-ayv-c-13-0-UI-s1 NCI_CGAP_E11 Homo sapiens cDNA clone
IMAGE:5844036 3', mRNA sequence.
BQ002730
BQ002730.1 GI:19727630
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 673)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

source

Location/Qualifiers
1..673
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5844036"
/clone_lib="NCI_CGAP_E11"
/tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/note="Organ: Left Pelvis; Vector: p7T3-Pac (Pharmacia)
with a modified polylinker; Site.1: EcoR I; Site.2: Not I;
NCI_CGAP_E11 is a normalized cDNA library containing the
following tissue(s): Chondrosarcoma. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into p7T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dr)18 tail. The sequence tag for this library is
ACACTGTCAC.
TAG_LIB=UI-H-E11
TAG_TISSUE=chondrosarcoma
TAG_SEQ=ACACTGTCAC"

BASE COUNT

ORIGIN

183 a 144 c 147 g 198 t 1 others
Query Match 11.0%; Score 635.8; DB 14; Length 673;
Best Local Similarity 99.2%; Pred. No. 1.3e-111;
Matches 659; Conservative 0; Mismatches 3; Indels 2; Gaps 2;
Qy 3505 CGGGCAGGTGCGAACCTTATGGCAGCAGCCAGGACATTGGCTGGAGGACTACACGG 3564
Db 673 CGGGCAGGTGCGAACCTTATGGCAGCAGCCAGGACATTGGCTGGAGGACTACACGG 614
Qy 3565 CCTATAGTGGCAGCTGACTCAGAGGCCAAGCCGATACATCAGAGCTCTAGTGCATG 3624
Db 613 CCTATAGTGGCAGCTGACTCAGAGGCCAAGCCGATACATCAGAGCTCTAGTGCATG 554
Qy 3625 AAGGAAACAGGTGATGCGAGACTCAGGACCTATCTATGACCAACCTACGCTGCGGGC 3684
Db 553 AAGGAAACAGGTGATGCGAGACTCAGGACCTATCTATGACCAACCTACGCTGCG- GGC 495

Search completed: December 27, 2002, 04:35:08
Job time : 4912 secs

QY 3685 GGCTGGGTCTATTCTCTCTCAAGAAATGGTCTATTCTCTCAGACCTCAAGTACGAAT 3744
Db 494 GGCTGGGTCTATTCTCTCTCAAGAAATGGTCTATTCTCTCAGACCTCAAGTACGAAT 436
QY 3745 GCAGAGATATTTAAACAAGATTGCTGCTATTCGCGCAATGCCCTGTGCATGCCATGGTC 3804
Db 435 GCAGAGATATTTAAACAAGATTGCTGCTATTCGCGCAATGCCCTGTGCATGCCATGGTC 376
QY 3805 CCTAGACACCTCAGTTTCATTGTTGGTCCCTTGGGCTTCTCTCTAGCAGCACCTCCTGTC 3864
Db 375 CCTAGACACCTCAGTTTCATTGTTGGTCCCTTGGGCTTCTCTCTAGCAGCACCTCCTGTC 316
QY 3865 CTTGACCTTAACTCTGATGGTTCTTCCACCTCCTGCCAGCAACCCCAACCAAGTGCCT 3924
Db 315 CTTGACCTTAACTCTGATGGTTCTTCCACCTCCTGCCAGCAACCCCAACCAAGTGCCT 256
QY 3925 TCAGAGGATAATATCAATGGAACCTCAGAGATGAACATCTAACCCACCTAGAGGAACACG 3984
Db 255 TCAGAGGATAATATCAATGGAACCTCAGAGATGAACATCTAACCCACCTAGAGGAACACG 196
QY 3985 TTTGGTGATATATGAGACTTTTATGTGGAGTGAATAATGGGATGCCATTACATTTGCTTTT 4044
Db 195 TTTGGTGATATATGAGACTTTTATGTGGAGTGAATAATGGGATGCCATTACATTTGCTTTT 136
QY 4045 TCTGTTTGTGTTTAAAGAAGTACGCTTTTACATATATAAATGTAATTAATTTATTTAT 4104
Db 135 TCTGTTTGTGTTTAAAGAAGTACGCTTTTACATATATAAATGTAATTAATTTATTTAT 76
QY 4105 GTGTATATGGAGTTCAAGGGAATCTGTGCATAGCCATTATGATAAATTAGCATGAAA 4164
Db 75 GTGTATATGGAGTTCAAGGGAATCTGTGCATAGCCATTATGATAAATTAGCATGAAA 16
QY 4165 AATA 4168
Db 15 AATA 12